GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

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Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                         Database
                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OM protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein search, using sw model
 SPTREMBL_21:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_phage:*
11: sp_virus:*
12: sp_virus:*
13: sp_virus:*
14: sp_unclassifie
15: sp_bacteriap:*
17: sp_archeap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-867-753-2
986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            671580 seqs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MARSLVHDTVFYCLSVYQVK.....LMLANELRADPDDCVYIVVD 184
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
                                                                                                                                                                                                       sp_invertebrate:*
                                                                                                                                                      sp_organelle:*
                                                                                                                                                                                                                                                                                                                                                                                                                                              671580
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	15	14	13	12	11	10	9	8	7	6	5	4	ω	2	1	Result No.
186	187	188	188.5	190	191.5	191.5	196	197	197	212	212.5	216	216	260.5	789	Score
18.9	19.0	19.1	19.1	19.3	19.4	19.4	19.9	20.0	20.0	21.5	21.6	21.9	21.9	26.4	80.0	Query Match Length DB
563	328	227	371	640	562	248	314	387	382	286	227	288	288	137	148	ength I
G	13	11	Ç	σ	4	13	11	11	11	σ	11	4	4	4	4	B
Q9VTX6	Q9W7M5	070238	061282	Q8T0M4	Q96QS3	012952	054817	Q9Z2U3	088933	Q8T6I5	Q9EQM5	Q9BQY4	Q9BR00	Q9Y4W1	095030	ID
Q9vtx6 drosophila	Q9w7m5 brachydanio	070238 mus musculu	O61282 hemicentrot	Q8t0m4 drosophila	Q96qs3 homo sapien	Ol2952 cynops pyrr	O54817 mus musculu	Q9z2u3 mus musculu	O88933 mus musculu	Q8t6i5 branchiosto	Q9eqm5 mus musculu	Q9bqy4 homo sapien	homo	Q9y4w1 homo sapien	095030 homo sapien	Description

45	44	43	42	41	40	39	38	37	36	3 5	34	33	32	31	30	29	28 .	27	26	25	24	23	22	21	20	19	18	17
173	174	174	174	174.5	175	175.5	175.5	176	176	176	176	176	176	176	176.5	177	177.5	179	179	179	179.5	180	180	180	180	181	182.5	183
17.5	17.6	17.6	17.6	17.7	17.7	17.8	17.8	17.8	17.8	17.8	17.8	17.8	17.8	17.8	17.9	18.0	18.0	18.2		18.2		18.3	18.3	18.3	18.3	18.4	18.5	18.6
210	464	295	282	350	484	371	228	835	612	612	479	479	370	214	493	387	276	826	391	301	362	299	299	299	240	365	185	408
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Q9QYR0	Q9NDA9	Q968Z4	073678	Q9IAL2	Q9CZK7	046169	062546	Q96н85	Q26441.	Q24477	013081	Q9CXI6	Q25411	Q8UVD3	Q9ES16	093582	Q98TG7	Q9BI30	Q8T8C1	046170	Q21836	Q9JLT8	Q9WTQ9	Q8SQ03	Q8R4I3	Q9GMA3	P79857	Q9VPP1
Q9qyr0 stochomys 1	Q9nda9 branchiosto	Q968z4 hemicentrot	073678 oryzias lat	. Q9ial2 gallus gall		046169 tribolium c	062546 hydra atten	Q96h85 homo sapien		Q24477 drosophila	013081 coturnix co	Q9cxi6 mus musculu	Q25411 lineus sang	Q8uvd3 gallus gall			Q98tg7 gallus gall	Q9bi30 ciona intes	Q8t8c1 gryllus bim	046170 tribolium c	Q21836 caenorhabdi	Q9jlt8 rattus norv	. Q9wtq9 rattus norv	Q8sq03 canis famil	Q8r4i3 mus musculu	Q9gma3 bos taurus		Q9vpp1 drosophila

ALIGNMENTS

Qy Db	Qu Be	SQ	FΤ	DR	DR K	DR	DR	DR	RL	RA	RP	RN	RĽ	RT	RA	RΡ	RN	×	8	8	SO	GN	DE	ΡŢ	Dī	DΤ	AC	IJ	RESULT 095030
1 MARSLVHDTVFYCLSVYQVKISPTPQLGAASSAEGHVGQGAPGLMGNMNPEGGVNHENGM 60 	Ouery Match 80.0%; Score 789; DB 4; Length 148; Best Local Similarity 100.0%; Pred. No. 6.3e-63; Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	SEQUENCE 148 AA; 16143 MW; 7C81BD318E70825C CRC64;	NON_TER 148 148	PROSITE; PS50071; HOMEOBOX_2; 1.	Figure Proude; nomeobox; 1. SMART; SM00389; HOX; 1.	InterPro: IPR001356; Homeobox.	HSSP; P06601; 1FJL.	EMBL; AC005023; AAC78617.1;	Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.		SEQUENCE FROM N.A.	. [2]	Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.	"The sequence of Homo sapiens BAC clone GS1-42113.";	Leonard S., Graves T., Cofman M.;	SEQUENCE FROM N.A.	[1]	NCBI_TaxID=9606;	Primates; Catarrhini; Hominidae;	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens (Human).		protein ((TrEMBLrel. 19,	(TrEMBLrel. 10,	1999 (TrEMBLrel.	095030;	O95030 PRELIMINARY; PRT; 148 AA.	LT 1 30

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RESULT
Q9BR000
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Q9BR000
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Best Local :
                                                                                                                                                                                                                                                        Q9BR00;
01-JUN-2001
01-JUN-2001
01-MAR-2002
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SEQUENCE FROM N.A. Howell G.R., Huckl
                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                            Hypothetical 31.6 kDa protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                              Q9BR00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -I- SUBCELLULAR LOCATION: NI
EMBL; AL049631; CAB46720.1;
HSSP; P06601; 1FJL.
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Homo sapiens (Human).
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DJ513M9.1 (Novel homeobox domain protein) (Fragment).
                                                                                              NCBI_TaxID-9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00027; HOMEOBOX_1; 1. PROSITE; PS50071; HOMEOBOX_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00028; ProDom; PD000010;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000047; HTH_repress
InterPro; IPR000327; POU_domain.
Pfam; PF00046; homeobox; 1.
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KPEQQQEEPPLLELKQEQEEPPQTTVEGPQPAEGPQTAEGPQPPERKRRRRTAFTQFQLQ 74
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137 AA;
                                                                                                                                                                                                                                                        (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 20, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Huckle
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16126 MW; 9B2E9CF358E59ABC CRC64;
                                                                                                                                                       Chordata;
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Ε.
                                                                                                                               Primates;
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47.5%;
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Ross
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 260.5;
Pred. No. 7.
M . T
                                                                                                                            Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                              288
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hes 28;
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                                                                                                                                                                                                                                                           update)
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RESULT 4 .
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Best Local
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Q9BQY4;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
Q1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 20, Last annotation update)
Q1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 31.7 kDa protein (CDNA FLJ25396 fis, cl
'unmanbox protein) (Homeobox protein from AL590526).
                                                                                                                                                                                 Hotute T., Hiraoka S., Murakawa K., Takiquchi S., Kusano J., Watanabe M., Fujimori K., Tanaal H., Ishida M., Yamashita H., Chiba Suzuki Y., Hata H., Nakagawa K., Mizuno S., Worinaga M., Kawamura M. Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A. Kawakami B., Nagai K., Isogai T., Sugano S.;
"NEDO human cDNA sequencing project.";
"NEDO human cDNA sequencing project.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
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SMART; SM0389; HOX; 1.
PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
EMBL; AL590524; CAC36517.1; -.
HSSP; P06601; 1FJL.
               Strausberg R.;
                              SEQUENCE FROM N.A.
TISSUE=TESTIS;
                                                                                                                                        TISSUE=TESTIS;
                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                        TISSUE-TESTIS;
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                      Submitted
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. Howell G.R., Huckl
                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA-binding; Homeobox; Hypothetical protein; Nuclear procedures 288 AA; 31637 MW; 50B571B13DB712B9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001356; Homeobox.
InterPro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                       "Molecular cloning
                                                                                                                                                                                                                                                                                          (shibashi T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157
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                                                                    Y., Jin Y., Levine A.J.; lecular cloning and characterization of a novel testis homeobox e, THG1, as a potential testicular tumor suppressor gene."; mitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
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 (JAN-2002)
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Chordata;
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Pred. No. 1.7e
23; Mismatches
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EMBL/GenBank/DDBJ
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Best Local
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9EQM5;
Q9EQM5;
01-MAR-2001
                                                                                                                                                                                                                         Takasaki N., McIsaac R., Dean J.;

"Gpbox, a novel homeobox gene preferentially expressed in cells at the onset of sexual dimorphism in mice.";

Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF201698; AAG36768.1;

EMBL; AF201698; AAG36768.1;

MGD; MGI:1925663; 1600026001Rik.

InterPro; IPR001356; Homeobox.

Pfam; PF00046; homeobox; 1.
                                                                                                                                                            ProDom; PD000010; Homeobox; 1.

SMART; SM00389; HOX; 1.

PROSITE; PS50071; HOMEOBOX_2; 1.

SEQUENCE 227 AA; 25112 MW; D39CF6795AF682DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
EMBL; AL590556; CAC36519:1; -.
EMBL; AK058125; BAB71675:1; -.
EMBL; AK058125; BAB71675:1; -.
EMBL; BF317219; AAL02160:1; -.
EMBL; BC021719; AAH21719:1; -.
HSSP; P06601; 1FJL.
                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                            Homeobox protein GPBOX.
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01-MAR-2001 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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SMART; SM00389; HOX; 1.
PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
PROSITE; PS00215; MITOCH_CARRIER;
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InterPro; IPR001993; Mitoch_carrier.
Pfam; PF00046; homeobox; 1.
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    114
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DNIQEEGGENIDQQPPQQEAAIPE----GMRNPQAGNYLAHQRTRRTRFTHSQLRDLER
                                                                                   GAASSAEGHVGQGAPGLMGNMNP-----EGGVNHENGMNRDGGM-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QFPSEFLRRRLARSMNVTELAVQIWFENRRAKWRRHQRALMARNML
                                                         GGLDQGEGAQGEVAGGEQAQEEPAPLSPAQEATGGEEEGENKEGEMEGRHAGDGASGPED
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58; Conserv
                                                                                                                              Similarity
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ox; Hypothetical protein; Nucleon 131691 MW; 2B0E007064515808
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34.9%; Pr
ative 23;
                                                                                                              21.6%; Score 212.5; 35.7%; Pred. No. 2.70 tive 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         16,
20,
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Last sequence update)
Last annotation update)
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Pred. No. 1.7e-11;
3; Mismatches 57
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                                                                                                                        .7e-11;
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808 CRC64;
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RESULT 7
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O88933;
O1-NOV-1998 (TIEMBLIEL CO1-NOV-1998 (TIEMBLIEL CO1-JUN-2002 (TIEMBLIEL CO1-JUN-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2002
01-JUN-2002
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jackman W.R. Jr., Kimmel C.B.;
"Coincident iterated gene expression in the amphioxus ne submitted (JAN-2002) to the EMBL; GenBank/DDBJ databases EMBL; AF465939; AALB3210.1; -.
Homeobox; DNA-binding; Nuclear protein.
SEOUENCE 286 AA; 31551 MW; 6BF50B62D92958C1 CRC64;
                       SEQUENCE FROM N.A.

MEDLINE=97392770; PubMed=9245514;

MITHESE PROJUBLY PRO
                                                                                                                                                                                                                           Mech.
                                                                                                                                                                                                                                                             "Spx1, a novel X-linked spermatogenesis.";
                                                                                                                                                                                                                                                                                                                           MEDLINE-97398449; PubMed-9256347; Branford W.W., Zhao G.Q., Valeriu Birkenmeier E.H., Rowe L.B., Pott
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Branchiostoma floridae (Florida lancelet) (Amphioxus).
Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
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52; Conservative
188:85-95(1997).
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(TrEMBLrel.
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B., Potter S.S.
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nscription factor Shox.
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Best Local Similarity
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MGD; MGI:L096388; ESx1.
InterPro; IPR001356; Homeobox.
InterPro; IPR000047; HTH_repressr.
Pfam; PF00046; homeobox; 1.
PRINTS; PR00031, HTHEPRESSR.
PRODOM; PD000010; Homeobox; 1.
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Q9Z2U3;
01-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
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SEQUENCE FROM N.A.
Branford W.W., Pot
                                                                      MGD;
                                                                                                                           Activity of the ESX1 Homeoprotein.";
Mol. Cell. Biol. 20:661-671(2000).
-!- SUBCELLULAR LOCATION: NUCLEAR (BEMBL; AF017734; AAD01621.1; -.
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PROSITE; PS50071; HOMEOBOX_2; 1.
DNA-binding; Homeobox; Nuclear p
SEQUENCE 382 AA; 43540 MW; EV
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                                                                                                                                                                                                                                                                                                                             MEDLINE-20079279; PubMed-10611245;
                                                                                                                                                                                                                                                                                                                                                                     STRAIN-129
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     placenta."
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                                                                                                       HSSP;
                                                                                                                                                                                                                                                             Yan Y.T., Stein S.M., Ding J., Shen M.
"A Novel PF/PN Motif Inhibits Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ESX1 OR EPX
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MGI:1096388; Esx1.
erPro; IPR001356; Hc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LMQPVAQSSPQPLPANPLQAPQQPEEQEEEEEEQPGEEQPQQE-PKPRRYRICFTPIQLQ
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AF017735;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 10, Last sequence update) (TrEMBLrel. 21, Last annotation update) protein EPX (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata;
Rođentia;
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   Homeobox.
HTH_repressr
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the EMBL/GenBank/DDBJ databases
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Pred. No. 1
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Sciurognathi; Muridae;
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                                                                                                                                                                SIMILARITY)
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01-MAR-2002
Paired-like
                                                                                                             PROSITE; PS00027; HÓMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
DNA-binding; Homeobox; Nuclear p
SEQUENCE 314 AA; 35969 MW; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProDom; PD000010; Homeo SMART; SM00389; HOX; 1
                                                                                                                                                                                                                      TRANSFAC; T03474; ...
MGD; MGI:1096388; Esx1.
InterPro; IPR001356; Homeobox.
InterPro; IPR000047; HTH_repressr.
                                                                                                                                                                                                                                                                                                                                                      "Esxl, a novel X c
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                                                                                                                                                                     ProDom; PD000010; Homeobox; 1. SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                             Dev. Biol. 188:85-95(1997).
-!- SUBCELLULAR LOCATION: NUCLEAR
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Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                               PRINTS; PR00031; HTHREPRESSR.
                                                                                                                                                                                                               Pfam; PF00046; homeobox;
                                                                                                                                                                                                                                                                                              EMBL; AF004211; AAB94670.1;
                                                                                                                                                                                                                                                                                                                                       extraembryonic tissues and male germ
                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97392770; PubMed=9245514;
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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YQEPEGFEPSRGEAAAP--
                           YQVKISPTPQLGAASSAEGHVGQGAPGLMGNMNPEGGVNHENGMNRDGG---
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                                                                                                                                                                                                                                                                                 P06601; 1FJL.
                                                                                                                                                                                                                                                                                                                                        Lemaire P., Behringer R.R.;
Lemaire P., Behringer R.R.;
a novel X chromosome-linked homeobox gene expressed
a novel X chromosome rank cells.";
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                                                       . Similarity 59; Conserv
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                                                                    19.9%;
34.1%;
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20, Last annotation update)
containing protein.
 VAEAPQAWNGNENLGGGFLEANAQLGEADAAPVRQSLMRP
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                                                      Score 196; DB 11;
Pred. No. 1.2e-09;
8; Mismatches 72;
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Pred. No. 1.2e-09;
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                                                                                                            protein.
72568F81DA4AA246 CRC64;
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012952;
01-JUL-1997
01-NOV-1998
01-MAR-2002
  Q96QS3;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
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PROSITE; PS50071; HOMEOBOX_2; 1.
DNA-binding; Homeobox; Nuclear protein.
DNA-binding; Homeobox; Nuclear protein.
SEQUENCE 248 AA; 27687 MW; 98BDBA7D61DB59D6 CRC64;
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SMART; SM00389; HOX; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-96136334; PubMed-8573168; Takabatake T., Takahashi T.C., In "Activation of two Cynops genes,"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sone K., Takeshima K., Takahashi T., Dev. Genes Evol. 207:147-155(1997).
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                                                                                                                                                                                               Q
R
                                                                                                                                                                                                                                                                       --RTRRTKFTLLQVEELESVFRHTQYPDVPTRRELAENLGVTEDKVRVWFKNKRARCRRH 161
                                                                                                                                                 줐
                                                                                                                                                                                                                                           RKRRHRTIFTDEQLEALEHLFQETKYPDVGTREQLARRVHLREEKVEVWFKNRRAKWRRQ
                                                                                                                                                                                                                                                                                                                                                 SCVPAPSSG
                                                                                                                                                                                                                                                                                                                                                                                          GMIPEGGGGNQEPRQQPQPPPEEPAQAAMEGPQPENMQP------ 103
                                                                                                                                                                                                                                                                                                                                                                                                                                           YPRALGPTAGLPTLAGSKVGYNGGYYYGQLHLQPPGAPGCCGAMQPLGA-----QQC 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YQVKISPTPQLGA-ASSAEGHVG------QGAPGLMGNMNPEGGVNHENGMNRDG 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELESVFRHTQYPDVPTRRELAENLGVTEDKVRVWFKNKRARCRRHQRELMLAN 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LMQPVAQSSPQPLPANPLQAPQQPEEQEEEEEEQPGEEQPQQE-PKPRRYRICFTPIQLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -MIPEGGGGNQ----EPRQQPQPP----PEEPAQAAMEGPQPENMQPRTRRTKFTLLQVE 116
                                                                                                                                                                                               163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 29.7
54; Conservative
                                                                                                                                                 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR001356; Homeobox.
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                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208,
                                                                                                                                                                                                                                                                                                                                          -YDGSSSVLMSPMPHQMMPYMNVGTLSRSELQLLNQLHCR 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19;
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Last sequ
Last anno
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9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 191.5; DB 13; Length Pred. No. 2.2e-09;
                         PRT;
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s, fork head and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence update) annotation update)
                         562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Takabatake
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .2e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54;
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RESULT 12
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Best Local
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01-JUN-2002
01-JUN-2002
                                                                                                                                                                                                                                                                                                   Q8TOM4;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C. Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wa Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AY069177; AAL39322.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ohira R.H., Zhang Y.H., Guo W., Dipple K., Shih S., Doerr J Huang B.-L., Fu L., Abu-Khalil A., Geschwind D., McCabe E.; "Human ARX gene: genomic characterization and expression."; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AY038071; AAK93901.1;
                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; MuscEphydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                               STRAIN-BERKELEY;
                                                                                                                              SEQUENCE FROM
                                                                                                                                                                                                                 Drosophila
                                                                                                                                                                                                                                             GH22493p.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA-binding; Homeobox; Nuclear protein. NON_TER 562 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001356; Homeobox.
InterPro; IPR003654; Homeo_OAR.
Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aristaless-related homeobox Homo sapiens (Human).
                                                                                                                                                         NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00027; PROSITE; PS50071;
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[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                       336
                                                                                                                                                                                                                                                                                                                                                                                                                   111
                                                                                                                                                                                                                                                                                                                                                                                                                                             278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19 VKISPTPQLGAASSAEGHVGQGAPGL----MGNMNPEGGVNHEN---GMNRDGGMIPEG
                                                                                                                                                                                                                                                                                                                                                                                                    TLLQVEELESVFRHTQYPDVPTRRELAENLGVTEDKVRVWFKNKRARCRRHQR 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LKISQAPQV-SISRSKSYRENGAPFVPPPPALDELGGPGGVTHPEERLGVAGGPGSAPAA 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGGTGTEDDEEEELLEDEEEELLEDDEEEELLEDDARALLKEPRRCPVAATGAVAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGN--
                                                                                                                                                                                                                                                                                                                                                                                     TSYQLEELERAFQKTHYPDVFTREELAMRLDLTEARVQVWFQNRRAKWRKREK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAAAVATEGGELSPKEELLLHPEDA--EGKDGEDSVCLSAGSDSEEGLLKRKQRRYRTTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                              melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          562 AA;
                                                                                                                                                                                                                                                       (TrEMBLrel.
(TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                          N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HOMEOBOX_1; UNKNOWN_1.
HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58159 MW;
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Last annotation update)
                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 191.5;
Pred. No. 5.8
                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FBDF41E387C65532 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                  640
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                                                                                                                                                                                                                                                        update)
                                                                                                                                                                                  Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91;
                                                       ge R.,
C.J.,
Wan K.,
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8

Query Match

19.3%;

Score 190;

DB

5;

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                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O61282 PRELIMINARY; PRT; 371 AA.
O61282; PREMBLrel 07, Created)
O1-AUG-1998 (TrEMBLrel 07, Last sequence update)
O1-MAR-2002 (TrEMBLrel 20, Last annotation update)
                                                                                                                                                                                                                        DNA-binding; Homes
371 AA;
                                                                                                                                                                                                                               PROSITE; PS00027; HOMEOBOX.1; 1.
PROSITE; PS50071; HOMEOBOX.2; 1.
DNA-binding; Homeobox; Nuclear p;
SEQUENCE 371 AA; 41272 MW; 61
                                                                                                                                                                                                                                                                                                                                                                                        "Two isoforms of orthodenticle-related proteins (Henhancer element of sea urchin arylsulfatase gene. Dev. Biol. 181:284-295(1997).

-I- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE=97166044; PubMed=9013937;
                                                                                                                                                                                                                                                                                         SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                             EMBL; AB011526; BAA28675.1; HSSP; P06601; 1FJL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sakamoto N., Akasaka K., Mitsunaga-Nakatsubo K., Takata
Nishitani T., Shimada H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Orthodenticle-related protein.
                                                                                                                                                                                                                                                                                                     PRINTS; PR00024; HOMEOBOX.
ProDom; PD000010; Homeobox; 1.
                                                                                                                                                                                                                                                                                                                                 Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (FEB-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shimada H., Akasaka K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=7650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Echinoidea; Euechinoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hemicentrotus pulcherrimus (Sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HPOTXE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113
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                                                                                                                                           14 LSVYQVKISPTPQLGAASSAE-----GHVGQGAPGLMGNMNPEGGVN------
                            TRRTKFTLLQVEELESVFRHTQYPDVPTRRELAENLGVTEDKVRVWFKNKRARCRRHQRE 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LQVEELESVFRHTQYPDVPTRRELAENLGVTEDKVRVWFKNKRARCRRHQR 163
RERTTETRAQLDVLETLESRTRYPDIEMREEVAMKINLPESRVQVWEKNRRAKCRQQQQQ
                                                         AYSNPMYGEGALPAPDRHVPP---TQQHPMFQPQVLGPMTSERPHSNGVDPPRKQ----R 132
                                                                                   -HENGMNRDGGM-----IPEGGGGNQEPRQQPQ----PPPEEPAQAAMEGPQPENMQPR 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EQLDELEKEFDKSHYPCVNTREKLAARTALSEARVQVWFSNRRAKWRRHQR 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGRLSLPALSPDSGS-----RDSRSPDADANRMIDIEGEDSESQDSDQPKFRRNRTTFSP 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------MIPEGGGGNQEPRQQPQPPPEEPAQAAMEGPQPENM---QPRTR--RTKFTL 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TPPGGGPAGAGGALQPGGSGSSYGSDGNMSSNPNSSNSNTTHSNGHNTNSGSGCGDSSAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TPQLGAASSAEGHVGQGAPGLM----GNM--NP---EGGVNHENGMNRDGG------
                                                                                                               LNVKPMKLE---RVGMSSSPPRLTIDCGNTGRSP--VPSHMEPPGGARVPYPMHLYPYQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 32.: 55; Conservative
                                                                                                                                                                                       Similarity
                                                                                                                                                                          Conservative
                                                                                                                                                                                      19.1%;
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                                                                                                                                                                          34;
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                                                                                                                                                                                         Score 188.5;
Pred. No. 6.
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                                                                                                                                                                                                                                 protein.
6F4BEF71251E5EF7 CRC64;
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                                                                                                                                                                                       No.
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ches 60;
                                                                                                                                                                       i.6e-09;
ies 53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Takata K.,
                                                                                                                                                                         Indels
                                                                                                                                                                                                  Length 371;
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                                                                                                                                                                      Gaps
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 192
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RESULT 14
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Best Local
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01-MAY-1999
01-MAR-2002
Danio rerio.";
Danio rerio.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
-I- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
EMBL; AF071496; AAD42021.1; -.
                                                                                                                                                                                                                                                 Q9W7M5;
                                                                                                                             Actinopterygii; Neopterygii; Cyprinidae; Danio.
                                                                                                                                        Brachydanio rerio (Zebrafish) (Zebra danio)
Eukaryota; Metazoa; Chordata; Craniata; Ver
Actinopterygii; Neopterygii; Teleostei; Ost
                                                                                                                                                                                                         01-NOV-1999 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00046; homeobox; 1.
ProDom; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
SEQUENCE 227 AA; 25484 MW; 0FEF5EC1C5EAE374 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Han Y.J., Park A.R., Seong I Submitted (JAN-1999) to the EMBL; AF017453; AAD08781.1; HSSP; P06601; LFJL.
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                                                              Del Giacco L., Di Benedetto B., "Isolation of the mRNA encoding
                                                                                                                            Cyprinidae;
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                                                                                                                                                                                            Orthopedia protein.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                       SEQUENCE FROM N.A.
                                                                                                                NCBI_TaxID=7955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSFAC; T03294; -.
MGD; MGI:1202888; Psx1.
InterPro; IPR001356; Homeobox.
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207:159-166(1998).
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55; Conservative
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9 (TrEMBLrel.
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R., Sung D.Y., Chun J.Y.;
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to the EMBL
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Sciurognathi; Muridae;
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Otp (
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murinae; Mus
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Search completed: April 28, 2003, 03:35:05 Job time: 74 secs
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R ZFIN; ZDB-GENE-990708-7; otp.

R InterPro; IPR001355; Homeobox.

R InterPro; IPR001354; Homeobox.

R InterPro; IPR000364; HTH_repressr.

R InterPro; IPR000047; HTH_repressr.

R Pfam; PF00046; homeobox: 1.

R PRINTS; PR00031; HTHREPRESSR.

R PRINTS; PR00031; HTHREPRESSR.

R PRODOm; PD00010; Homeobox; 1.

R PROSITE; PS00027; HOMEOBOX_1; 1.

R PROSITE; PS00027; HOMEOBOX_2; 1.

R PROSITE; PS00027; HOMEOBOX_3; 1.

R PROSITE; PS00027; HOMEOBOX_3; 1.
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ALIGNMENTS

C;Accession: JC6522
R;Qu, S.; Li, L.; Wisdom, R.
Gene 203, 217-223, 1997
A;Title: Alx-4: cDNA cloning and characterization of a novel
A;Reference number: JC6522; MUID:98086222; PMID:9426253
A;Contents: Embryo

paired-type homeodomain

paired-type homeodomain protein, Alx-4 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 31-Mar-2000

JC6522

A;Cross-references: GB:AF001465; NID:g2352265; PIDN:AAC39943.1; PID:g2352266 C;Comment: This protein belongs to the family of paired-type homeodomain proteins, C;Genetics:

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A;Accession: JC6522 A;Molecule type: mRNA A;Residues: 1-399 <QUA>

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homeotic protein goosecoid [validated] - human c; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 01-Sep-2000 C; Accession: A54677 R; Blum, M.; De Robertis, E.M.; Kojis, T.; Heinzmann, C.; Klisak, I.; Geissert, D.; Genomics 21, 388-393, 1994 Genomics 221, 388-393, 1994
                                                                                                                                RESULT 2
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C;Superfamily: homeotic protein Hox B3; homeobox homology
C;Keywords: DNA binding; embryo; homeobox; nucleus; transcription regulation
F;203-259/Domain: homeobox homology <HOX>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                  GKKRRNRTTFTSYQLEELEKVFQKTHYPDVYAREQLAMRTDLTEARVQVWFQNRRAKWRK
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30.1%;
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 homeobox gene goosecoid (GSC) and mapping of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
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homeobox protein Pmx - mouse
N;Alternate names: homeotic protein K-2b
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
                                                                                    RESULT 4
148902
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A;Map position: 14q32.1-14q32.1
C;Superfamilly: homeotic protein goosecoid; homeobox homology C;Keywords: DNA binding; homeobox; nucleus; transcription reg;156-212/Domain: homeobox homology <HOX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Reference number: A54677; MUID:94375063; PMID:7916327
A;Accession: A54677
A;Status: preliminary; not compared with conceptual transposed type: DNA
A;Molecule type: DNA
A;Residues: 1-252 <BLU>
C;Genetics:
A;Gene: GDB:GSC
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A;Title: Gastrulation in the mouse: the role of the homeobox gene goosecoid A;Reference number: A42768; MUID:92315328; PMID:1352187

A;Accession: A42768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Mus musculus (house mouse)
C;Datc: 10-Sep-1999 #sequence_revision 10-Sep-1999
C;Accession: A42768
R;Blum, M.; Gaunt, S.J.; Cho, K.W.Y.; Steinbeisser,
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A;Note: sequence extracted from NCBI backbone (NCBIP:108110)
C;Superfamily: homeotic protein goosecoid; homeobox homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-256 <BLU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
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Best Local
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Best Local
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                                                                                                                                                                                                        QR
                                                                                                                                                                                                                                                                                       --RTRRTKFTLLQVEELESVFRHTQYPDVPTRRELAENLGVTEDKVRVWFKNKRARCRRH 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             homeobox homology <HOX>
                                                                                                                                                                                                                                                                                                                             -QQCSCVPTPPGYEGPGSVLVSPVPHQMLPYMNVGTLSRTELQLLNQLHCR
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Pred. No. 2.8e-07
6; Mismatches 3
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Pred. No. 2.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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C;Accession: 17000; R;Kern, M.J.; Argao, E.A.; R;Kern, M.J.; Argao, E.A.; Genomics 19, 334-340, 1994
                                                                                C; Keywords: alter
F; 95-151/Domain:
                                                                                                                                                                                                                                                                                                                                                              homeotic protein K-2a - mouse
C;Species: Mus musculus (house mouse)
C;Date: 25-Feb-1994 #sequence_revision 01-Sep-1995 #text_change 24-Sep-1999
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                                                                                                                                                                                                                                       A; Reference number: A; Accession: S26076
                                                                                                                                                                                                                                                           A; Title: A novel murine homeobox gene isolated by a tissue specific PCR cloning A; Reference number: S26076; MUID:93027261; PMID:1383943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Вb
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A; Residues: 1-217 <KER>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: A novel murine
A;Reference number: S260
A;Accession: S26077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Kern, M.J.; Witte, D.P.; Valerius, M
Nucleic Acids Res. 20, 5189-5195, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Title: MHox:a mesodermally restricted homeodomain protein A; Reference number: I53118; MUID:93083424; PMID:1360403 A; Accession: I53118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:U03873; NID:g460124; PIDN:AAC52139.1; PID:g460125 R;Cserjesi, P.; Lilly, B.; Bryson, L.J.; Wang, Y.; Sassoon, D.A.; Olson, E Development 115, 1087-1101, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-217 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Title: Genomic organization and chromosome localization A; Reference number: I48902; MUID:94245205; PMID:7910581
                                                                                                                                               A; Experimental source: fetal heart
                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-245 <KER>
                                                                                                                                                                                                                                                                                                                          R; Kern, M.J.;
                                                                                                                                                                                                                                                                                                                                            C; Accession: S26076
                                                                                                                                                                                                                                                                                                                                                                                                                                      $26076
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:L06502; NID:g199583; PIDN:AAA39672.1; R;Kern, M.J.; Witte, D.P.; Valerius, M.T.; Aronow, B.J.; Poti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-217 <RE2>
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                                                                                                                                                                      A;Cross-references: EMBL:X59725; NID:g51361;
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                                                                                                       Superfamily: unassigned homeobox proteins; homeobox homology; Keywords: alternative splicing; DNA binding; homeobox; nucle
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                                          Query Match
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  L Similarity
49; Conser
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                                                                                                                                                                                                                                                                                                                          Witte, D.P.; Valerius, M.T.;
                                                                                     homeobox
  Conservative
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                    18.7%;
29.0%;
                                                                                     homology
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29.0%; Pred. No. 2.86
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  27;
                    Score 184.5;
Pred. No. 3.
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    Mismatches
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                                                                                                                                                                                                                                                                                                                            Aronow,
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                                                                                                                                                                        PIDN: CAA42410.1;
                    2e-07;
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ter, S.S.
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                                                                                                                                                                        PID:g51362
39;
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A46403
                                                           C; Function:
                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-419 <HAH>
                                                                                                                                                                                                                                                                              A; Title: Drosophila goosecoid participates A; Reference number: S70617; MUID:96272167; A; Accession: S70617
                                                                                                                                                                                                                                                                                                                                                       R; Hahn, M.; Jaeckle, H.
EMBO J. 15, 3077-3084,
                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Drosophila melanogaster
C;Date: 10-Sep-1999 #sequence_revi
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A;Reference number: A46403;
A;Accession: A46403
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Genes Dev. 7, 114-129, 1993
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                                                                                   A; Map position:
                                                                                                          A; Cross-references:
                                                                                                                               A; Gene: gsc
                                                                                                                                                                                 A; Cross-references: EMBL: U52968;
                                                                                                                                                                                                                                                       A; Status: nucleic acid sequence not
                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N; Alternate names:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 homeotic
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A; Residues: 1-384 <SCH>
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       Description: plays
Note: not required
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AENLGVTEDKVRVWFKNKRARCRRHQR 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTNSPVSDGNSDCEADEYAPK---RKQRRYRTTFTSFQLEELEKAFSRTHYPDVFTREEL
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                                                                                                          FlyBase:FBgn0010323
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     a role in neurogenesis in post-gastrula for gastrulation like Xenopus goosecoid;
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                                                                                                                                                                                 NID: g1399586;
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Pred. No. 6.8e-07;
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                                                                                                                                                                                 PIDN: AAB17948.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69;
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                                                                                                                          R;Thomas, P.Q.; Johnson, B.V.; Rathjen, J.; Rathjen, P.I.
J. Biol. Chem. 270, 3869-3875, 1995
A;Title: Sequence, genomic organization, and expression
A;Reference number: A55882; MUID:95181349; PMID:7876132
A;Accession: A55882
                                                                                                                                                                                                                                          N;Alternate names: homeotic protein HES-1
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change C;Accession: A55802; S35540; Parking T. Parking D. C;Accession: A55802; S35540; Parking T. Parking T. Parking D. C;Accession: A55802; S35540; Parking T. Parking T. Parking D. C;Accession: A55802; S35540; Parking T. P
RESULT
A55882
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A:Introns: 43/3; 85/1; 147/2; 162/3; 222/1
C:Superfamily: unassigned homeobox proteins
C:Keywords: DNA binding; homeobox; nucleus
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C;Keywords: DNA binding; homeobox; r
F;287-343/Domain: homeobox homology
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                                                                           A; Molecule type: mRNA
A; Residues: 1-185 < THO>
                                                                                                                                                                                                                                                                                                                                                     homeobox protein Hesxl - mouse
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A; Residues: 1-362 <WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VEELESVERHTQYPDVPTRRELAENLGVTEDKVRVWFKNKRARCRRHQR 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NHENGMNRDGGMIPEGGGGNQEPRQQPQPPPEEPAQAAMEGPQPENMQPRTRRTKFTLLQ 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LDELEKVFARTHYPDVFTREELATRVQLTEARVQVWFQNRRAKYRKQER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ly: unassigned homeobox proteins; homeobox homology
DNA binding; homeobox; nucleus; transcription regu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source: clone R08B4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #sequence_revision 15-Oct-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL: Z68008; PIDN: CAA92001.1; GSPDB: GN00028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18.2%;
35.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RKRRHRTIFTEEQLEQLEATFDKTHYPDVVLREQLALKVDL 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 1.20
5; Mismatches
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Pred. No. 1.2e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                November
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                                                    PID:g510537
                                                                                                                                                                              novel homeobox
                                                                                                                                                                                                                                                                              24 - Sep - 1999
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C; Superfamily: unusury...
C; Keywords: DNA binding; homeobox; nucleus
F; 109-165/Domain: homeobox homology <HOX>
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C;Date: 21-Sep-1993 #sequence_revision 10-May-1996 #text_change 17-Mar-1999
C;Accession: A45452; A56744; B45452
В
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C;Superfamily: paired box transcription factor Pax-3; homeobox homology;
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;67-123/Domain: homeobox homology <HOX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Hoth, C.F.; Milunsky, A.; Lipsky, N.; Sheffer, R.; Clarren, S.K.; Baldwin, C.T. Am. J. Hum. Genet. 52, 455-462, 1993
A;Title: Mutations in the paired domain of the human PAX3 gene cause Klein-Waardenburg A;Reference number: A45452; MUID:93190976; PMID:8447316
A;Accession: A45452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Macina, R.A.; Barr, F.G.; Galili, N.; Rie Genomics 26, 1-8, 1995
A;Title: Genomic organization of the human A;Reference number: A56744; MUID:95301273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
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A; Residues: 1-28;43-326 <MAC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Note: sequence modified after extraction from NCBI backbone A; Note: sequence extracted from NCBI backbone (NCBIN:126845, 1 R; Macina, R.A.; Barr, F.G.; Galili, N.; Riethman, H.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-28,29-306 <HOT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transcription factor PAX3 - human (fragments)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: EMBL:L02646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 116-151 <
                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: A56744
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Best Local S
Matches 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;Gene: GDB:PAX3; WS1
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Best Local
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124
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                                                                                                                                                                                                                                                                                          Local Similarity
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QAGANQLMAFNHL
                                            H--QRELMLANEL 171
                                                                                                                                                                                                                      GMIP---EGGGGNQEPRQQPQPPPEEPAQAAMEG------PQ-----PEN 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRRTKFTLLQVEELESVFRHTQYPDVPTRRELAENLGVTEDKVRVWFKNKRARCRRHQRE 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GNSEKDGNPPLHAPDLPSETSFPCPVDHPRPEERAPKYENYFSASETRSLKRELSWYRGR 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GNQE----PRQQPQPPPEEPAQAAMEGPQPENMQP-----
                                                                                        RKQRRSRTTFTAEQLEELERAFERTHYPDIYTREELAQRAKLTEARVQVWFSNRRARWRK
                                                                                                                                                                               GAVPRMMRPGPGQNYPRS--GFPLEKKAKHSIDGILSERASAPQSDEGSDIDSEPDLPLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  GDB:120495; OMIM:148820; OMIM:193500
136
                                                                                                                                                                                                                                                                                          18.0%;
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                                                                                                                                                                                                                                                                        16;
                                                                                                                                                                                                                                                                                          Score 177; DB 2; Pred. No. 1.6e-06;
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PMID:7782066
                                                                                                                                                                                                                                                                                                             Length 326
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                                                                                                                                                                               63
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C;Superfamily: unassigned homeobox proteins; homeobox homology C;Keywords: DNA binding; homeobox; nucleus; transcription regu F;95-151/Domain: homeobox homology <HOX>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Kuratani, S.; Martin, J.F.; Wawersik, S.; Lilly, B.; Eichele, G.; Olson, E.N. Dev. Biol. 161, 357-359, 1994
A;Title: The expression pattern of the chick homeobox gene gMHox suggests a role A;Reference number: I51226; MUID:94148118; PMID:7906232
A;Accession: I51226
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F;182-238/Domain: homeobox homology <HOX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Reference number: I49265; MUID:91265334; A;Accession: I49265
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C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #tex
                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-154, 156-245 < NOH>
                                                                                                                                                                                                                                                                                                           A; Reference number: A; Accession: I50413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Gallus gallus (chicken)
C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 17-Nov-2000
C;Accession: I51226; I50413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mech. Dev. 33, 27-37, 1990 A; Title: The murine paired
                                                                                                                                                                A;Gene: gMHox; Prx-1
                                                                                                                                                                                           C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-245 <KUR>
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                                                                                                                                                                                                              A;Cross-references: GB:D13433; NID:g222850; PIDN:BAA02695.1;
                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
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Matches
                     Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preliminary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KRKQRRSRTTFTAEQLEELEKAFERTHYPDIYTREELAQRTKLTEARFQVWFSNRRARWR 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGGVNHENG------MNRDGGMIPEGGGGNQEPRQQPQPPPEEPAQAAMEGPQPE 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preliminary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RHORELMLANELRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NMQPRTRRTKFTLLQVEELESVFRHTQYPDVPTRRELAENLGVTEDKVRVWFKNKRARCR 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGDKKEEDGEKKAKHSIDGILGDKGNRLDEGSGVESEP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L Similarity
45; Conserv
                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17.9%;
33.6%;
17.8%; Score 176; DB 2; 32.9%; Pred. No. 1.4e-06; cive 21; Mismatches 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene paired-related protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 176.5;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-Jul-1996 #text_change 02-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        is expressed
PMID:1982921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.6e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                specifically
                                                                                                                                                                                                                                                                                                                                                       paired
                                                                                                                    regulation
                                                                                                                                                                                                              PID:g222851
                                                                                                                                                                                                                                                                                                                                                                                                     PID:g545360
H.; Saito, T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---DLPL 177
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                                                                                                                                                                                                                                                                                                                                                       predominantly
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                                                                                                                                                                                                                                                                                                                                                                                                          T.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the
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                                                                                                                                                                                                                                                                                                                                                         expr
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Indels

38;

Gaps

<u>ب</u>

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A;Gene: Phox2
C;Superfamily: unassigned homeobox proteins;
C;Keywords: DNA binding; homeobox; nucleus; t
F;91-147/Domain: homeobox homology <HOX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: Psx C;Superfamily: mouse placenta-specific homeobox protein; homeobox homology C;Superfamily: mouse placenta-specific homeobox protein; homeobox homology C;Keywords: DNA binding; homeobox; nucleus; placenta; transcription regulation F;151-207/Domain: homeobox homology <HOX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     placenta specific-homeobox protein - mouse C:Species: Mus musculus (house mouse) C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 C:Accession: JC6540 R:Han, Y.J.: Park, A.R.: Sung, D.Y.: Chun, J.Y.: Gene 207, 159-166, 1998 A:Title: Psx, a novel murine homeobox gene expresse A:Reference number: JC6540; MUID:98172748; PMID:951 A:Accession: JC6540
                                                                                                                                                                                                                                                                                                                       Phox2 homeodomain protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #text_change 24-Sep-1999
C:Accession: I48713
C:Accession: I48713
                                                                                                                          A;Cross-references: EMBL:X75014; NID:g402641; PIDN:CAA52923.1; C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      망
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A; Residues: 1-247 <HAN>
A; Cross-references: GB:AF017453
C; Comment: This protein is involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
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                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-280 < RES>
                                                                                                                                                                                                                               A; Reference number: A; Accession: I48713
                                                                                                                                                                                                                                                A; Title: The mouse homeodomain protein Phosa; Reference number: I48314; MUID:94244481;
                                                                                                                                                                                                                                                                                         R;Valarche, I.; Tissier-Seta, J.P.; Hirsch, M.R.; Martinez, S.; Goridis, C.; Brunet, Development 119, 881-896, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                         A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             150 WFKNKRARCRRHQRELM 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMEGPQPEN--MQPRTRRTKFTLLQVEELESVFRHTQYPDVPTRRELAENIGVTEDKVRV 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FKNKRARCRRHQRELMLANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WFRMRRALFQRNRRVLM 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGRHAGDGA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EG-HVGQGAPGLMGNMNPEGGVNHENGMNRDGGMIPEGGGG-NQEPRQQPQPPPEEPAQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FONRRAKFRRNER-AMLASK 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VNHENGMNRDGGMI----PEGGGGNQEPRQQPQPPPEEPAQAAMEG-----PQPEN 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIRNPHVLNRLAQLRYRRTRFTHSQLHDLERLFQETRYPSLRARRDLARWMGVDECDVQN 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DQLNSEEKKKRKQRRNRTTFNSSQLQALERVFERTHYPDAFVREDLARRVNLTEARVQVW 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MQ-----PRTRRTKFTLLQVEELESVFRHTQYPDVPTRRELAENLGVTEDKVRVW 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VSHLLDLEEAGDMVAAQGDEGGG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17.8%;
    17.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---SSSEDDSILEEGGQNIDQQPPQQEAASPD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 176; DB 1;
Pred. No. 1.4e-06;
                                                                                                                                                                                                         from GB/EMBL/DDBJ
  Score 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in controlling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                Phox2 regulates Ncam promoter activity in concert 481; PMID:7910552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expressed in PMID:9511757
                                                            transcription regu
  DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -EPGRSLLESPGLTSGSDTPQQDN
  2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 247;
Length 280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                            regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   during
                                                                                                                                             PID: 9402642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Ωy
                                                                              Вb
                                                                                                                                                                                                                                                    C;Superfamily: unassigned homeobox proteins;
C;Keywords: DNA binding; homeobox; nucleus;
F;47-171/Domain: paired box homology <PBH>
                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X95594; NID:g1296835; PIDN:CAA64847.1; A;Note: the authors translated the codon GCC for residue 338 as C;Comment: This factor is a key regulator of eye morphogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Loosli, F.; Kmita-Cunisse, M.; Gehring, W.J.
Proc. Natl. Acad. Sci. U.S.A. 93, 2658-2663, 1996
A;Title: Isolation of a Pax-6 homolog from the ribbonworm
A;Reference number: JC6130; MUID:96181462; PMID:8610097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                paired box transcription factor Pax-6 - Ribbonworm C;Species: Lineus sanguineus (ribbonworm) C;Date: 16-Apr-1997 #sequence_revision 09-May-1997 C;Accession: JC6130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δÃ
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  В
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                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-370 <LOO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           몽
                                                                                                                                                                                                                                    F;270-326/Domain: homeobox homology <HOX>
                                                                                                                                                                                                                                                                                                               A; Introns: 162/3; 236/2; 287/1; 314/3
                                                                                                                                                                                                                                                                                                                                                   C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: JC6130
                                                                                                                                                                                                                                                                                                                                 A; Gene: Pax-6
                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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  285
                                        119
                                                                              225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23
                                                                                                                                                                           Local Similarity
                                                                                                       ESVFRHTQYPDVPTRRELAENLGVTEDKVRVWFKNKRARCRRHQRELMLANELR 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TEARVQVWFQNRRAKFRKQER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TEDKVRVWFKNKRARCRRHQR 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPPEEPAQAAMEGPQPENMQPRTRRTKFTLLQVEELESVFRHTQYPDVPTRRELAENLGV 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTPQLGAASSAEGHVGQGAPGLMGNMNPEGGVNHENGMNRDGGMIPEGGGGNQEPRQQPQ 82
EKEFERTHYPDVFARERLAQKIDLPEARIQVWFSNRRAKWRREEK----LRNQRR 335
                                                                              QPQPPPISPTKKESDGHSSADSHSGDTPNGNESEEQMRIRLKRKLQRNRTSFTNAQIEAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCPALGSSNCALGALRDHQPA----PYSAVPYK---
                                                                                                                                                         40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31.2%; --- 22;
                                                                                                                                                                           17.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----RRIRTTFTSAQLKELERVFAETHYPDIYTREELALKIDL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           150
                                                                                                                                                       16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 1.7e-06;
                                                                                                                                                                           Score 176; DB 2;
Pred. No. 2.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-May-1997 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                        homeobox homology; paired transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----FFPEPSGLHEKRKQ---
                                                                                                                                                                                              Length 370;
                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lineus
                                                                                                                                                           24;
                                                                                                                                                                                                                                                                                                                                                                     It plays a role in
                                                                                                                                                                                                                                                                                                                                                                                                            PID:e222109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sanguineus
                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90
                                                                              284
                                                                                                                                                                                                                                                                                           box homology
                                                                                                                                                                                                                                                                                                                                                                                                          PID:g129
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

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                                             Sequence 30, Application US/08957351 Patent No. 6306586
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GENERAL INFORMATION:
APPLICANT: Semina
APPLICANT: Murray
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                           101 LTEARVRVWFKNRRAKWRKRER 122
                                                                                                                                                                        142 VTEDKVRVWFKNKRARCRRHQR 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142 VTEDKVRVWFKNKRARCRRHQR 163
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                                                                                                                                                                                                                                       86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: UI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 24-OCCCLASSIFICATION: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41
                                                                                                                                                                                                     41 SEKASASLPGGSPEDGSLKKKQRRQRTHFTSQQLQELEATFQRNRYPDMSTREEIAVWTN 100
                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                           313 amino acids
Semina,
Murray,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        617-832-7000
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                                                                                                                                                                                                                                                                                                                                19.3%; Score 190.5; DB 4 ilarity 34.5%; Pred. No. 1.5e-11; Conservative 23; Mismatches 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Semina,
                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                          protein
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            Elena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jeffrey C.
Jeffrey C.
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                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                    CORRESPONDENCE ADDRESS:
SOFTWARE:
              OPERATING SYSTEM:
                                                                                       COUNTRY:
                                                                                                            STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                         41
                                                                                                                                                      ADDRESSEE:
                                                                            02109-2170
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Boston ž

USA

SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30

E: FOLEY, HOAG & ELIOT One Post Office Square

HOAG & ELIOT LLP

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US-08-957-351-3
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                                                                                         Sequence 3, Application US/08957351 Patent No. 6306586 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 34.5
Matches 49; Conservative
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ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,
REFERENCE/DOCKET NUMBER:
                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
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MEDIUM TYPE: Floppy disk
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NUMBER OF SEQUENCES:
                 TITLE OF INVENTION:
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STREET: C...
STREET: C...
TWY: Boston
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                                                                                                                                                                                                                                                                   142 VTEDKVRVWFKNKRARCRRHQR 163
                                                                                                                                                                                                                                                                                                                                            86 EEPAQAAMEGPQPEN----MQPRTRRTKFTLLQVEELESVFRHTQYPDVPTRRELAENLG 141
                                                                                                                                                                                                                                                                                                                                                                                                                        26 QLGAASSAEGHVGQGAPGLMGNMNPEGGVNHENGMNRDGGMIPEGGGGNQEPRQQPQPPP 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 24-OCT
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                                                       Murray,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           617-832-7000
                                                                         Semina,
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               Jeffrey C.
METHODS AND COMPOSITIONS FOR THE
DIAGNOSIS AND TREATMENT OF CATARACTS
                                                                           Elena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19.2%;
34.5%;
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Pred. No. 1.9e-11;
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RESULT 6
US-08-957-351-27
; Sequence 27, Application US/08957351
; Patent No. 6306586
; GENERAL INFORMATION:
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; ORGANISM: mouse
US-09-129-888-2
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                                     Matches
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APPLICANT: HAN, Yun Jeong
TITLE OF INVENTION: Placenta trophoblast-specific gene
FILE REFERENCE: 1942/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/129,888B
CURRENT FILING DATE: 1998-08-06
NUMBER OF SEO ID NOS: 6
SOFTWARE: WordPerfect 6.1 Windows
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: UII
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
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                                                                                                                                 197
                                                                                                                                                            150 WFKNKRARCRRHQRELM 166
                                                                                                                                                                                              137 SIRNPHVLNRLAQLRYRRTRFTHSQLHDLERLFQETRYPSLRARRDLARWMGVDECDVQN 196
                                                                                                                                                                                                                                                              99 EGRHAGDGA----- 136
                                                                                                                                                                                                                                                                                            34 EG-HYGQGAPGLMGNMNPEGGVNHENGMNRDGGMIPEGGGG-NQEPRQQPQPPPEEPAQA 91
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CLASSIFICATION:
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                                                                                                                               WFRMRRALFQRNRRVLM 213
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Pred. No. 2.6e-11;
""^matches 31; Indels
                                                                                                                                                                                                                                                                                                                                                 Score 176; DB 3;
Pred. No. 3.3e-10;
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US-08-957-351-26
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                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                      APPLICANT: Semina, Elena
APPLICANT: Murray, Jeffrey C.
TITLE OF INVENTION: METHODS A
TITLE OF INVENTION: DIAGNOSIS
                                                                                                                                                                             ADDRESSEE: FOLEY, HC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 315 amino acids
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                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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APPLICANT: Murray, Jeffrey C.
                                                                                                                                                                                                                                                                                                                                                                                                                       110 QRNRYPDMSMREEIAVWTNLTEPRVRVWFKNRRAKWRKRERNQQL 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 DGGMIPEGGGGNQEPRQQPQPPPEEPAQAAMEGPQPENMQPRTRRTKFTLLQVEELESVF 122
                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 DGGAGSAGCGGG------AEDPA-----KKKKQRRQRTHFTSQQLQELEATF 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Arnold, Beth E. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                               ZIP:
                                                                                                                                                              STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/957,351
FILING DATE: 24-OCT-1997
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                                                                                                            COUNTRY:
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                                                                                                                                                                           ADDRESSEE:
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o. 6306586
                                                                                           02109-2170
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APPLICATION DATA:
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37.1%;
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                                                                                                                                                                                                                           METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND TREATMENT OF CATARA
                                                                                                                                                                           HOAG & ELIOT LLP
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               Release #1.0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 173.5;
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APPLICATION NUMBER: FILING DATE: 24-OCT

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US/08/957,351

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RESULT 8
US-08-775-009-37
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Best Local S
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APPLICANT: Gong,
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                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                        REFERENCE/DOCKET NUMBER: CH
TELECOMMUNICATION INFORMATION:
                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Y
                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 617-832-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: No. 5935783el Genes Mapping TITLE OF INVENTION: Veliocardiofacial Syndrome N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Roe, Bruce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 ESVFRHTQYPDVPTRRELAENLGVTEDKVRVWFKNKRARCRRHQR 163
TYPE: amd TOPOLOGY:
                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 27-DE CLASSIFICATION: 43
                                                                                                                                                                                                                                                  SOFTWARE:
                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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REFERENCE/DOCKET NUMBER: UIA-024.01
                                                                                                                                       REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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                                                                                       TELEPHONE:
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                             LENGTH:
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No. 5935783
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                                                                                                                                                     Trujillo, Doreen Yatko
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36.2%;
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Pred. No. 1.7e-09;
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; LOCATION: (117)..(177)
; OTHER INFORMATION: homeobox
US-09-636-735A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Berg, Patricia
TITLE OF INVENTION: NO. 641695
FILE REFERENCE: 179.37405X00
CURRENT APPLICATION NUMBER: US
CURRENT FILING DATE: 2000-08-
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                                                                        SOFTWARE: PatentIn version SEQ ID NO 12 LENGTH: 240
                                                                                                                                                                                                                                                                   Sequence 12, Application US/09636735A Patent No. 6416956
                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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Best Local Similarity
Matches 45; Conserv
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LENGTH: 240
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Best Local Similarity
Matches 40; Conserv
                                                                                                                                                  APPLICANT: Berg, Patricia
TITLE OF INVENTION: No. 6416956el Transcription Factor,
FILE REFERENCE: 179.37405X00
CURRENT APPLICATION NUMBER: US/09/636,735A
CURRENT FILING DATE: 2000-08-11
                                                                                                                                NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.0
                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Homo sapiens
                  FEATURE:
NAME/KEY: HELIX 1
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                                                                                                                                                                                                                                                                                                                                                                                       130 QHLNQRFQHTQYLALPERAQLAAQLGLTQTQVKIWFQNKRSKYKK 174
                                                                                                                                                                                                                                                                                                                                                                                                                             116 EELESVFRHTQYPDVPTRRELAENLGVTEDKVRVWFKNKRARCRR 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 SVYQVKISPT----PQLGAASSAEGHV------GQGAPG--LMGNMNPE------GGVN 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HENGMNRDGGMIPEGGGGNQEPRQQPQPPPEEPAQAAMEGPQPENMQPRTRRTKFTLLQV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HPQELEAD-----SEKPRLSPEPSERRPQAPAKKLRKP-----
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27.3%;
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Pred. No. 1.1e-08;
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Pred. No. 8.6e-09;
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LOCATION: (127). NAME/KEY: HELIX

(127)..(136)

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Query Match
Best Local Similarity 52...
Best Local Similarity 52...
Conservative
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US-08-775-009-38
                                                                                             US-08-775-009-38
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Patent No. 5
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                                                                                                                                                                                                            TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: HELIX 3
LOCATION: (158)...
                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yatko
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CH-0681
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                              MOLECULE TYPE:
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: No. 5935783el Genes Mapping in the TITLE OF INVENTION: Vellocardiofacial Syndrome Minimal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 QHLNQRFQHTQYLALPERAQLAAQLGLTQTQVKIWFQNKRSKYKK 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116 EELESVFRHTQYPDVPTRRELAENLGVTEDKVRVWFKNKRARCRR 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: One Liver CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/0 FILING DATE: 27-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                             STRANDEDNESS: single
                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56 HENGMNRDGGMIPEGGGGNQEPRQQPQPPPEEPAQAAMEGPQPENMQPRTRRTKFTLLQV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29 AAYPLGLSPTTAASPNL-SYSRPYGHLLSYPYTEPANPGDSYLSCQQPAALSQPLCGPAE 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 SVYQVKISPT----PQLGAASSAEGHV------GQGAPG--LMGNMNPE------GGVN 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 16.3%;
Local Similarity 27.3%;
ses 45; Conservative
                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                LENGTH:
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                                                                                                                                                                           amino acid
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                                                                                                                                                                                            60 amino acids
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                                                                                                             internal
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Pred. No. 1.1e-08; ~
Prematches 52;
                         Score 160; DB 2;
Pred. No. 2.2e-09;
2; Mismatches 16;
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                                                         Length 60
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Critical Region
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                                                              ; MOLECULE TYPE: protein US-08-958-642-4
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US-08-958-642-4
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LENGTH: 99
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    Matches
                   Query Match
Best Local
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APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/031,962D
CURRENT FILING DATE: 1998-02-27
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Jennifer A. Price
TITLE OF INVENTION: Methods and Compositions for Enhancing
TITLE OF INVENTION: Osseous Growth, Repair, and Regeneration
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                                                                                                                                                           INFORMATION FOR SEQ ID NO:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NO
TITLE OF INVENTION: DII
NUMBER OF SEQUENCES: 19
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                               FILING DATE:
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 Local Similarity es 41; Conserv
                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                            LENGTH:
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es 31; Conserv
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                                                                                                                            436 amino acids
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                16.0%;
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    18;
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Score 158; DB 2; L
Pred. No. 4.7e-08;
Pred. No. 4.7e-08;
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                                                                                                                                                                                                                                                                         Version #1.30 (EPO)
                                Length 436;
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   Indels
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40 GAPGLMGNMNPEGGVNHENGMNRDGGMIPEGGGGNQEPRQQPQPPPEEPAQAAMEGPQPE 99

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US-08-778-423A-4
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US-08-778-394-2
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Best Local Similarity 30.8
                                                                                                                                                                                                                    Sequence 4, Application US/08778423A Patent NO. 6071697
GENERAL INFORMATION:
APPLICANT:
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TITLE OF INVENTION: NOVEL METHOD FOR TESTING THE TITLE OF INVENTION: DIFFERENTIATION STATUS IN PANCREATI NUMBER OF SEQUENCES: 16

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/778,423A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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FILING DATE:
CLASSIFICATION: 514
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                                                                                                                                                   NOVEL METHOD FOR TESTING THE DIFFERENTIATION STATUS IN PANCREATIC CELLS OF A MAMMAL
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Search completed: April 28, 2003, 04:05:27 Job time: 33 secs
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Best Local Similarity
Matches 41; Conserv
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 436 amino acids
                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein
                                                                    281
                                                                                                160 RHORELMLANELR 172
                                                                                                                                                                                                    184 GQPTQDGCQQQEGGGENTNSISSNG-------EDSDEAQMRLQLKR 222
                                                                                                                                   223 KLQ--RNRTSFTQEQIEALEKEFERTHYPDVFARERLAAKIDLPEARIQVWFSNRRAKWR 280
                                                                                                                                                                   100 NMQPRTRRTKFTLLQVEELESVFRHTQYPDVPTRRELAENLGVTEDKVRVWFKNKRARCR 159
                                                                                                                                                                                                                                     40 GAPGLMGNMNPEGGVNHENGMNRDGGMIPEGGGGNQEPRQQPQPPPEEPAQAAMEGPQPE 99
                                                                REEK---LRNORR 290
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)GY: linear
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30.8%;
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Pred. No. 4.7e-08;
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                                                                                                                                                                                                                                                                                                    Length 436;
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Result
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Maximum DB
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Perfect score:
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ALX4_MOUSE
PIX3_ROUSE
PIX3_RAT
CRX_BOVIN
GSC_HUMAN
GSC_MOUSE
PMX1_MOUSE
                              RX_DROME
PIX2_MOUSE
HEX1_MOUSE
GSC_BRARE
ARX_MOUSE
PMX2_HUMAN
PAX7_MOUSE
                                                                                                                                                                                                                                          GSC_DROME
CRX_HUMAN
CRX_MOUSE
PIX2_HUMAN
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OTP_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                         AL_DROME
ALX4_HUMAN
OTP_PARLI
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DLX4_MOUSE
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RX2_CHICK
SHX2_MOUSE
OTX_STRPU
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  P43271
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P54821
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SHOX_HUMAN

;	45	44	43	42	41	40	39	38	37	36	35	34	
,	173	173	173.5	173.5	174.5	175	176	176	176	176	176	176.5	
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			093385 gallus gall										•

ALIGNMENTS

RESULT 1

8888	ននន	888	388	388	38	88	88	RL X	R	RT A	RX	ਨ ਨ	RN	RL.	R 2	장	RN	2 2	3 P	RA	R X	RC	RP	S S	8	2 6	GN	DE	Ŋ	בן בן	Ä	ID	SHX2
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way		-i- SIMILARITY: BELONGS TO THE PAIRED HOMEOBOX FAMILY. "BICOID" SUBFAMILY.	-I- DEVELOPMENTAL STAGE: Expressed during cranofacial development as		ī	as well as in face and body structure formation!- SUBCELLULAR LOCATION: Nuclear.	May tems		gene family and is expressed during heart development	"A new human homeobox gene OG12X is a member of the most conserved	MEDLINE=98133920; PubMed=9466998;	SEQUENCE OF 110-331 FROM N.A. (ISOFORM 2). TISSUE=Craniofacial;	116-331 EDOK W & /150505W 31	Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.	Strausberg R.:	SEQUENCE FROM N.A.		Proc. Natl. Acad. Sci. U.S.A. 95:2406-2411(1998).	a SHOX-related homeobox gen	Wash H., Ried T., Rappold G.A.;	MEDLINE=98131323; PUDMEC=9482898; Blaschke R.T., Monaghan A.P., Schiller S., Schechinger R., Rao F.,	D. B. C.	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).	NCBI_TaxID=9606;	ia; Primates; Catarrhini; Hominidae,	Homo sapiens (Human). Rukarvota: Metazoa: Chordata: Craniata: Vertebrata: Ruteleostomi:	SHOX2 OR SHOT OR OG12X.	Short stature homeobox protein 2 (Paired-related homeobox protein SHOT) (Homeobox protein Ogl2X).	(Rel. 41, Last annota	16-OCT-2001 (Rel. 40, Creaced) 16-OCT-2001 (Rel. 40, Last sequence update)		HUMAN STANDARD	SHX2_HUMAN

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noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/

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RESULT 2
RX2_CHICK
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Retinal homeobox protein Rx2 (CRax2).
                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
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                                                    Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
Archosauria; Aves; Neogn
SEQUENCE FROM N.A. MEDLINE-99345958; PubMed-10415362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified entities or send a
                                                                                                                                                         RX2_CHICK
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PROSITE; PS50071; HOMEOBOX_2; 1.
PROSITE; PS50803; OAR; 1.
Homeobox; DNA-binding; Developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AJ002367; CAA05341.1;
EMBL; AJ002368; CAA05342.1;
EMBL; BC008829; AA0108829.1;
EMBL; AF022654; AAC39662.1;
EMBL; AF023203; AAC39663.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00024; HOMEOBOX.
PRINTS; PR00031; HTHREPRESSR.
PRODOM; PD0000010; Homeobox; 1
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InterPro; IPR003654; Homeo_OAR.
InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSFAC; T04223; -
TRANSFAC; T04224; -
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                                                                                                                                                                                                                                                                                                                           24
                                                                                        OR RAX2.
                                                                                                                                                                                                            FDETHYPDAFMREELSQRLGLSEARVQVWFQNRRAKCRKQENQL
                                                                                                                                                                                                                        FRHTQYPDVPTRRELAENLGVTEDKVRVWFKNKRARCRRHQREL 165
                                                                                                                                                                                                                                                                                                                       TPQLGAASSAEGHVGQGAPGLMGNMNPEGGVNHENGMNRDGGMIPEGGGGNQEP-----
                                                                                                                                                                                                                                                                                                   GAAERSREPGSPRLTEVSPELKDRKEDAK-GMEDEGQTKIKQRRSRTNFTLEQLNELERL
                                                                                                                                                                                                                                                                     ----RQQPQPP-----PE-----EPAQAAMEGPQPENMQPRTRRTKFTLLQVEELESV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P06601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HGNC:10854; SHOX2.
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                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                        125
244
312
325
331
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equires a license agreement (email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       splicing.
140 199
313 326
60 86
235 246
115 115
                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                          ΑĄ,
                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homeobox; 1.
                                                    Chordata; Craniata; Vertebrata; Euteleostomi; Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                    125
244
312
325
                                                                                                                                                                                                                                                                                                                                                                                         34964 MW;
                                                                                                                                                                                                                                                                                                                                                          20.9%;
                                                                                                                                                                                                                                                                                                                                                                                   OAR.

POLY-GLY.

MISSING (IN ISOFORM SHOX2B).

E -> EGRKKPTKAEVQATLLLPGEAFRFL (IN RE
2).

E -> D (IN REF. 1; CAA05341).

P -> S (IN REF. 2).

D -> N (IN REF. 2 AND 3).

H -> L (IN REF. 3; AAC39663).

MW; 55431B073B3B2250 CRC64;
                                                                                                                                                                                                                                                                                                                                              22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALT_INIT.
ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                         Score 206; DB 1
Pred. No. 3e-08;
                                                                                                                                                         PRT;
                                                                                                                                                         317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein;
                                                                                                                                                       A
                                                                                                                                                                                                                                                                                                                                                                  1; Length 331;
                                                                                                                                                                                                                                                                                                                                              50;
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                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein;
                                                                                                                                                                                                                                                                                                                                              36;
                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                        REF.
                                                                                                                                                                                                                                                                             121
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RESULT 3
SHX2_MOUSE
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Best Local
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                       SHX2_MOUSE
P70390; P703
16-OCT-2001
16-OCT-2001
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00389; HOX; 1.

PROSITE; PS00027; HOMEDBOX_1; 1.

PROSITE; PS50071; HOMEDBOX_2; 1.

PROSITE; PS50803; OAR; 1.

Homeobox; DNA-binding; Developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ohuchi H., Tomonari S., Itoh H., Mikawa T., Noji S.; "Identification of chick rax/rx genes with overlapping expression during early eye and brain development."; Mech. Dev. 85:193-195(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003654; Homeo_OAR.
InterPro; IPR001356; Homeobox.
Pfam; PF00046; homeobox; 1.
ProDom; PD000010; Homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AB020318; BAA84749.1; -. HSSP; P06601; 1FJL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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SUBCELLULAR LOCATION: Nuclear (By similarity).

DEVELOPMENTAL STAGE: Expressed at stage 4 in the ectoderm, stage 6 in the anterior most neural plate, at stage 7 and anterior neural fold and at stage 9-10 in the evaginating vesicles. At stage 14, highly expressed in developing retination in find the large 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: CONTAINS 1 HOMEOBOX DOMAIN.
SIMILARITY: CONTAINS 1 OAR DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in infundibulum region.
SIMILARITY: BELONGS TO THE PAIRED HOMEOBOX FAMILY "BICOID" SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                     TYQLHELERAFEKSHYPDVYSREELAMKVNLPEVRVQVWFQNRRAKWRRQEKLEVSSMKL
                                                                                                                                                                                                                                                      QDSP
                                                                                                                                                                                                                                                                                                       RADP
                                                                                                                                                                                                                                                                                                                                                                                         LLQVEELESVFRHTQYPDVPTRRELAENLGVTEDKVRVWFKNKRARCRRHQRELMLANEL 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                    HCLPKGPAEPPPAEHQGRFQEPYCPGSASPELPAGDGGDGKPSDEEQPKKKHRRNRTTFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---PRQQPQPPPEE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AEGAFSLSAPAARSPGGNPSRLHSIEAILGFTKDDGLLGPFQPDGGAGSAKEAADKRGPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AEGHVGQGAPGLM----GNMNPEGGVNHENGMNRDGGMI----PEGGGGNQE-----
                                                                                                    P70369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
  1 (Rel. 40, C
1 (Rel. 40, L
2 (Rel. 41, L
ure homeobox
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122
294
300
317 #
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
                                                                                                                             STANDARD;
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181
307
304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34056 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20.5%;
Last sequence update)
Last annotation update)
x protein 2 (Homeobox pr
                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 202.5;
Pred. No. 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEAR LOCALIZATION SIGNAL (POTENTIAL). 10DDf1BEC9a24910 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OCTAPEPTIDE MOTIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----PAQAAMEGPQPENMQP----RTRRTKFT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein; Nuclear protein;
                                                                                                                             331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .1e-08;
.es 61;
                                                                                                                           ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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subsequent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ,317;
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MBL outstation -
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Short stature

(Homeobox protein

Og12X) (OG-12)

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Rovescalli A.C., Asoh S., Nirenberg M.W.;
"Cloning and characterization of four murine homeobox genes.";
Proc. Natl. Acad. Sci. U.S.A. 93;10691-10696(1996).
[3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc.
                    TRANSFAC: T03310; -- TRANSFAC: T04233; -- TRANSFAC: T04233; -- MGD; MGT: 1201673; Shox2.
InterPro: IPR003654; Homeo_OAR InterPro: IPR001356; Homeobox.
                                                                                          EMBL;
EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                    van Schaick H.S.A., Smidt M.P., van der Kleij A.A.M., Asoh S.,
                                                                                                                                                                           modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                      use
                                                                                                                                                                                                                 the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-BALB/c; TISSUE-Liver, and MEDLINE-97008065; PubMed-8855241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORMS 1 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Paired family homeodomain SHOX2 OR OG12X OR PRX3.
                                                                                                                                                                                                                                                                                                                                                                                       +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Semina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98133920; PubMed=9466998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEVELOPMENTAL EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 116-331 AND 235-331 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tissues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98058757; PubMed=9371788;
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                                                                                 HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               homeobox gene family and is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Homeobox gene Prx3 expression in rodent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "A new
                                                                                                                                                                send an email to license@isb-sib.ch).
                                                                                                                                                                                                   s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bloinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                               L; U66918; AAC52833.1; -.
L; U67055; AAC52834.1; -.
L; U65071; -; LANOTATED_CDS.
L; U65072; AAC52831.1; ALT_INIT.
L; U65072; AAC52832.1; ALT_INIT.
P; P06601; 1FJL.
                                                                                                                                                                                                                                                             SIMILARITY: CONTAINS 1 HOMEOBOX DOMAIN SIMILARITY: CONTAINS 1 OAR DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: May be a growth regulator and have a role in specifying neural systems involved in processing somatosensory information, as well as in face and body structure formation. May also have a role in heart development.
                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE PAIRED HOMEOBOX "BICOID" SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human homeobox gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Metazoa; Chordata;
Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genet. 7:415-422(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reiter R.S., Murray J.C.;
homeobox gene OG12X is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Mouse)
           homeobox; 1.
                                   Homeo_OAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kozak C.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rovescalli A.C., Luijten M
(ozak C.A., Nirenberg M.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Embryo;
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during
                                                                                                                                                                           (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                              There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 brain and
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g heart d
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opment in
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RESULT 4

OTX_STRPU
ID OTX_S
AC Q2641
DT 15-U

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q26417;
15-JUL-1998
15-JUL-1998
15-JUN-2002
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VARSPLIC
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gan L.,
Klein W.
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PROSITE; PS50071; HOMEOBOX_2; 1.
PROSITE; PS50803; OAR; 1.
Homeobox; DNA-binding; Developmental protein;
                 EMBL;
                                                          use by non-profit institu
modified and this statement
entities requires a license
or send an email to license@
                                                                                                                                                                                                                                                                                      Dev. Biol. 167:517-528(1995).

Dev. Biol. 167:517-528(1995).

TO THE TAANCC MOTIF WITH HIGH SPECIFICITY.

FUNCTIONS IN THE DEVELOPING EMBRYOS.

FUNCTIONS IN THE DEVELOPING EMBRYOS.

SUBUNIT: BINDS DNA AS A MONOMER.

SUBCELLULAR LOCATION: Nuclear.

SUBCELLULAR LOCATION: Nuclear.

DEVELOPMENTAL STAGE: FOUND INITIALLY IN ALL

EMBRYO, BUT GRADUALLY BECOMES RESTRICTED TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strongylocentrotus purpuratus (Purple sea urchin)
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; I
Echinoidea; Euechinoidea; Echinocea; Echinoida; St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA_BIND
                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTX_STRPU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=95180495; PubMed=7875376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=7668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strongylocentrotus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          purpuratus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "An orthodenticle-related protein
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                                                                                                                                                                                                                                                 ENDODERM CELLS.
SIMILARITY: BELONGS
                                                                                                                                                                                                                              "BICOID" SUBFAMILY
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  S76899;
P06601;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mao C.-A., Wikramanayake A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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331 AA;
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  AAB33568.1;
1FJL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 36, Created)
. 36, Last sequence update)
. 41, Last annotation updat
OTX (SPOTX).
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326
82
246
                                                              license@isb-sib.ch)
                                                                                                                             institutions as long
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                                                                                                     is not removed.
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Pred. No. 5.
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OAR DOMAIN.
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                                                                                    (See
                                                                                                                                                                                                                                                   HOMEOBOX
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D TO
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                                                                                                       Usage
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ORAL E
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HAVE ADDITIONAL
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                                                                                                                                                                                                                                                                                                                CLEAVING
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PIX3_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 52; Conserv
       -1- SUBCELULLAR LOCATION: Nuclear (By similarity).
-1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN DEVELOPING EYE LENS.
-1- DISEASE: MUTATIONS IN PITX3 APPEAR TO BE THE CAUSE OF THE ANTERIOR SECHEM MESCHYMAL DYSGENESIS (ASMD) AND AUTOSOMAL-DOMINANT CONGENITAL CATARACTS (ADCC). ASMD INCLUDES ALL MALFORMATIONS INVOLVING THE FIRST (CORNEAL ENDOTHELIUM AND TRABECULAR MESHWORK), SECOND (CORNEAL STROMA) AND THIRD (IRIS STROMA) MESENCHYMAL WAVES OF NEURAL CREST. THE ASMD PHENOTYPE IS CHARACTERIZED BY CORNEAL OPACITIES WITH OR WITHOUT IRIS ADHESIONS IN 100%, CATARACTS OF VARYING SEVERITY IN 100% AND OPTIC-NERVE BANORMALITIES IN 20% OF AFFECTED INDUIDUALS. ADCC IS CHARACTERIZED BY DOMINANT TRANSMISSION OF A PHENOTYPE CONSISTING OF BILATERAL CONCENTAL CATARACTS IN A MOTHER AND SON WITHOUT CLINICAL ANTERIOR-SEGMENT
                                                                                                                                                                                                                                                                                              Nat.
[2]
                                                                                                                                                                                                                    Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND VARIANT ADCC ASN-13.
TISSUB-Craniofacial;
MEDLINE=99282096; PubMed=9620774;
Semina E.V., Ferrell R.E., Mintz-Hittner H.A.,
Alward W.L.M., Reiter R.S., Funkhauser C., Daac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence upd
15-JUN-2002 (Rel. 41, Last annotation upd
pitultary homeobox 3 (Homeobox protein
PITX3 OR PTX3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
HOMEODOX; DNA-binding; Developmental protein; Nuclear protein.
DNA_BIND 131 190 HOMEOBOX.
SEQUENCE 371 AA; 41215 MW; B6BD493D684A33F7 CRC64;
                                                                                                                                                                                                                                                                TISSUE=Muscle;
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                        dominant cataracts
                                                                                                                                                                                                                                                                                                                                                       Murray J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00024; HOMEOBOX.
ProDom; PD000010; Homeobox; 1.
                                                                                                                                                                                                                                                                                                                                        "A novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIX3_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                       DEVELOPMENT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -HENGMNRDGGMIPEGGGGNQEPRQQPQPPPEEPAQAAMEGPQPENMQP----RTRRTKF
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                                                                                                                                                                                                                                                                                                                                        homeobox gene PITX3 is mutated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T02416; -. IPR001356; Homeobox.
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                                                                                                                                                                                                                                                                                                           taracts and ASMD.";
19:167-170(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Human).
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29.9%;
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Last annotation update)

The protein PITX3).
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Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                   Daack-Hirsch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164
                                                                                                                                                                                                                    LENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .110
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ALX4_MOUSE
ID ALX4_MOUSE
AC 035137;
DT 16-OCT-2001
DT 16-OCT-2001
DT 15-UN-2002
DE HOMEODOX PIC
GN ALX4.
OS MUS MUSCULUS
OC EUKATYOTA; h
OC MAMMAIAI:
CX MOBI_TAXID=1
RN [1]
RP SEQUENCE FR
RC STRALN=C57BI
RX MEDLINE=9801
                                                                                                                                                                                                                                                                                     Qy
                                                                                                                                                                                                                                                                                                               В
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                                                                                                                                                                                                                   RESULT
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                  16-OCT-2001
16-OCT-2001
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
  SEQUENCE FROM N.A. STRAIN=C57BL/6; TI MEDLINE=98086222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00027; HOMEOBOX_1; PROSITE; PS50071; HOMEOBOX_2; PROSITE; PS50803; OAR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD000010; Homeo SMART; SM00389; HOX; 1.
                                                    NCBI_TaxID=10090;
                                                                                             Mus musculus (Mouse)
                                                                                                                       Homeobox protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00024; HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00046; homeobox;.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003654;
InterPro; IPR001356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIM; 602669;
MIM; 107250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genew; HGNC:9006; PITX3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSFAC; T04311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homeobox; DNA-binding; Developmental protein; Nuclear protein;
                                                                                                                                                                                                                                                          101
                                                                                                                                                                                                                                                                                   142 VTEDKVRVWFKNKRARCRRHQR
                                                                                                                                                                                                                   σ
                                                                                                                                                                                                                                                                                                               41
                                                                                                                                                                                                                                                                                                                                          86
                                                                                                                                                                                                                                                                                                                                                                                              26
                                                                                                                                                                                                                                                                                                                                                                    N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: CONTAINS 1 HOMEOBOX DOMAIN SIMILARITY: CONTAINS 1 OAR DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE PAIRED HOMEOBOX "BICOID" SUBFAMILY.
                                                                                                                                                                                                                                                          LTEARVRVWFKNRRAKWRKRER
                                                                                                                                                                                                                                                                                                                             EEPAQAAMEGPQPEN----MQPRTRRTKFTLLQVEELESVFRHTQYPDVPTRRELAENLG
                                                                                                                                                                                                                                                                                                                                                                    EFGLLSEAEAR----SPALSLS---DAGTPHP-----QLPEHGCKGQEHSD-----
                                                                                                                                                                                                                                                                                                                                                                                            QLGAASSAEGHVGQGAPGLMGNMNPEGGVNHENGMNRDGGMIPEGGGGNQEPRQQPQPPP
                                                                                                                                                                                                                                                                                                              SEKASASLPGGSPEDGSLKKKORRORTHFTSQQLQELEATFQRNRYPDMSTREEIAVWTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF041339;
BC011642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P06601; 1FJL.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mutation.
                                                                                                                      (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
otein aristaless-like 4 (ALX-4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           302
                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA;
                                                                                                                                                                                         STANDARD;
 TISSUE=Embryo;
2; PubMed=9426253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC24502.1;
AAH11642.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
275
250
272
13
                                                                    Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                    19.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homeo_OAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WW.
                                                                                                                                                                                                                                                                                                                                                                                                                      23;
                                                                                                                                                                                                                                                          122
                                                                                                                                                                                                                                                                                     163
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 190.5; DB 1
Pred. No. 3.5e-07;
3; Mismatches 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OAR.
POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEAR LOCALIZATION S -> N (IN ADCC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /FTId=VAR_003767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HOMEOBOX.
                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1E5259206ABC2E87 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            It is produced through a collaboration informatics and the EMBL outstation -
                                                                                                                                                                                         399
                                                                                                                                                                                         A
                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                        45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                        25;
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                    40
                                                                                                                                                                                                                                                                                                                                                                                             85
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Best Local S
Matches 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene
                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                             ProDom; PD000010; Horsmart; SM00389; HOX; PR0SITE; PS00027; HO
                                                                                                                                                                                                                                                                                        Transcription
DNA_BIND 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF001465; AAC39943.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polydactyly.";
Development 125:2711-2721(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qu S., Tucker S.C.,
Wisdom R., Vogt T.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98301426; PubMed=9636085;
Qu S., Tucker S.C., Ehrlich J.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 homeodomain protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Alx-4: cDNA cloning and
                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003654; Homeo_OAR.
InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:108359; Alx4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSFAC; T02967; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Mutations in mouse Aristaless-like4 cause Strong's luxoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT LST GLN-206.
                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00046;
 103
                                140
                                                                                                                                                                                                                                                                                                                         omeobox;
                                                              80
                                                                                              95
                                                                                                                           23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REDUCTIONS AND DUPLICATIONS OF THE RADIUS, ABSENCE OF THE TIBIA, CRANICARCIAL DEFECTS, REDUCTION OF THE PUBIS, AND DORSAL ALOPECIA. SIMILARITY: BELONGS TO THE PAIRED HOMEOBOX FAMILY. SIMILARITY: CONTAINS 1 HOMEOBOX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEEN AT SEVERAL SITES INCLUDING CRANIOFACIAL REGION, FIRST BRANCHIAL ARCH AND ANTERIOR ASPECT OF THE LIMB BUD.

DISEASE: DEFECTS IN ALX4 ARE THE CAUSE OF STRONG'S LUXOID (LST) PHENOTYPE. AT HETEROZYGOSITY LST IS CHARACTERIZED BY PREAXIAL ABNORMALITIES OF THE HINDFEET AND, VERY RARELY, OF THE FOREFEET HOMOZYGOTES SHOW PREAXIAL POLYDACTYLY OF ALL FOUR LIMBS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BRAIN, HEART, INTESTINE, KIDNEY, LIVER, MUSCLE, SPLEEN AND TESTIS. DEVELOPMENTAL STAGE: EXPRESSED FROM E8.25 AND CONFINED TO MESENCHYMAL CELLS THROUGHOUT THE EMBRYO DEVELOPMENT. EXPRESSION IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE SPECIFICITY: EXPRESSED IN OSTEOBLASTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: BINDS DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEVELOPMENT.
                               VPCYAKESNLGEPELPPDSEPVGMDNSYLSVKETGAKGPQDRASAEIPSPLEKTDSESNK 199
                                                                                                                          PTPQ---LGAASSAEGHVGQGAPGLMGNMNPEGGVNHENGMNRDGGMIPEGGGGNQEPRQ 79
-- PRTRRTKFTLLQVEELESVFRHTQYPDVPTRRELAENLGVTEDKVRVWFKNKRARCRR
                                                                                              PTPQPPPAPPAPPAHLYLQRGA----CKTPPDGSLK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P06601;
                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                PD000010; Homeobox; 1.
                                                                                                                                                                                                                                                                                                  PS50803; OAR; 1.
; DNA-binding; Developmental protein; Nuclear
ption regulation; Activator; Disease mutation
                                                                                                                                                                                                                                                                                                                                                PS00027; HOMEOBOX_1; 1.
PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                         399
                                                                                                                                                                                                                                                         202
379
206
                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1FJL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wisdom R.;
                                                                                                                                                                                                                         A;
                                                                                                                                                                                                                                                                                                                                                                                                             homeobox; 1.
                                                              -QPPPEEPA-----QAAMEGPQ----PENMQ-----
                                                                                                                                                                                                                                                         261
392
206
                                                                                                                                                                                                                         42762 MW;
                                                                                                                                                                         19.2%;
30.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FACTOR INVOLVED IN SKULL AND LIMB
                                                                                                                                                                        Score 189.5;
Pred. No. 5.
                                                                                                                                                                                                                                     R -> Q (IN LST; ABOLISHES DNA BINDING TRANSCRIPTIONAL ACTIVATION).
                                                                                                                                                                                                                                                                      OAR.
                                                                                                                                                                                                                                                                                      HOMEOBOX.
                                                                                                                                                                                                                        2EDE19DDACA21D25 CRC64;
                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Levorse J.M., Flaherty L.A.,
                                                                                                                                                                         .5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of a
                                                                                                                                                                                       DB 1;
                                                                                                                                                           49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  novel paired-type
                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOT EXPRESSED
                                                                                                                                                           Indels
                                                                                          -LQEGSGGHNAALQ 139
                                                                                                                                                                                                                                                                                                                 protein;
                                                                                                                                                                                        399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXPRESSION IS
                                                                                                                                                           57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     outstation
                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIX3_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Murray J.C.;
Murray J.C.;
"A novel homeobox gene PITX3 is
"A novel homeobox gene PITX3 is
dominant cataracts and ASMD.";
dominant cataracts and ASMD.";
Nat. Genet. 19:167-170(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIX3_MOUSE 035160;
                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Event the European Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98282096; pubMed=9620774;
Semina E.V., Ferrell R.E., Mintz-Hittner H.A., Bitoun
Alward W.L.M., Reiter R.S., Funkhauser C., Daack-Hirso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1902 (Rel. 41, Last annotation update)
Pituitary homeobox 3 (Homeobox protein PITX3)
                                                                                            EMBL; AF005772;
HSSP; P06601; 1
                                                                                                                                                        modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nat. Genet. 19:16/-1/0(1998).
-!- FUNCTION: Appears to be involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Embryo, and Embryonic carcinoma; MEDLINE=97472463; PubMed=9328475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                           InterPro;
                                                                                                                                           or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           on mouse chromosome 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Isolation of a new homeobox gene belonging to the Pitx/Rieg family: expression during lens development and mapping to the aphakia region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Semina E.V., Reiter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEVELOPMENTAL EXPRESSION
                                                                             TRANSFAC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   260 RER 262
                                                                                                                                                                                                                                                                                                phenotype, a recessive homozygous eyes and closed eyelids.
SIMILARITY: BELONGS TO THE PAIRED "BICCOID" SUBFAMILY.
                                                                                                                                                                                                                                                                        SIMILARITY: CONTAINS 1 HOMEOBOX DOMAIN. SIMILARITY: CONTAINS 1 OAR DOMAIN.
                                                                                                                                                                                                                                                                                                                                        muscles.

DISEASE: Mutations in PITX3 appear to be the cause of the aphakia phenotype, a recessive homozygous disease characterized by small
                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE SPECIFICITY: Highly expressed in developing eye lens. DEVELOPMENTAL STAGE: First expressed in the eye in day E10 post-coitum embryos. Throughout eye development, expressed in lens placode and forming lens pit. From day E12, also detected the midbrain region, tongue, incisor primordia, condensing
                                                                                                                                                                                                                                                                                                                                                                                                    mesenchyme around the sternum and vertebrae and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GKKRRNRTTFTSYQLEELEKVFQKTHYPDVYAREQLAMRTDLTEARVQVWEQNRRAKWRK
                                                             MGI:1100498; Pitx3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lens development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163
                            IPR003654; Homeo_OAR IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genet. 6:2109-2116(1997).
                                                                                                                                         equires a license agreement (See http://www.isb-sib.ch/announce/email to license@isb-sib.ch).
                                                                                             1FJL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                           AAB87380.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murray J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mutated in
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                                                                                                                                                                          Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              anterior-chamber
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                                                                                                                                                                                                          restrictions
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                                                                                                                                                                                                                         EMBL
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                                                                                                                                                                                                                                       collaboration
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                                                                                                                                                                            commercial
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InterPro;

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                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-98058810; PubMed=9371841; Smidt M.P., van Shaick H.S.A., Lanctot C., Tremblay J.T., Cox van der Kleij A.A.M., Wolterink G., Drouin J., Burbach J.P.H. "A homeodomain gene Ptx3 has highly restricted brain expressinesencephalic dopaminergic neurons."; Proc. Natl. Acad. Sci. U.S.A. 94:13305-13310(1997).
TRANSFAC;
              EMBL; AJ011005; CAA09455.2; HSSP; P06601; 1FJL.
                                                                                          modified
                                                                                                      use
                                                                                                                      the
                                                                                                                                    between
                                                                                                                                                      This
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                                                                                                                                                                                                                                                           <del>-</del> <del>-</del> <del>-</del> <del>-</del>
                                                                                                                                                                                                                                                                                                                                 Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PITX3 OR PTX3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pituitary homeobox 3 (Homeobox protein PTX3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1998 (Rel. 36, 30-MAY-2000 (Rel. 39, 15-JUN-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P81062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIX3_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Hypothalamus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                  REVISIONS
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                                                                    s SWISS-PROT entry is copyright. It is produced through a copyre the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content is iffied and this statement is not removed. Usage by and fo ities requires a license agreement (See http://www.isb-sib.
                                                                                                                                                                                               SUBCELLULAR LOCATION: Nuclear.
TISSUE SPECIFICITY: Restricted to mesencephalic dc
system (MESDA).
SIMILARITY: BELONGS TO THE PAIRED HOMEOBOX FAMILY.
"BICCOID" SUBFAMILY.
SIMILARITY: CONTAINS 1 HOMEOBOX DOMAIN.
                                                                                                                                                                                 SIMILARITY: CONTAINS 1 HOMEOBOX DO SIMILARITY: CONTAINS 1 OAR DOMAIN.
                                                                                                                                                                                                                                                                                      FUNCTION: Appears to be involved in normal eye anterior-chamber and lens development. Transcription factor which may be involve in developmental determination of the mesda.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RHTQYPDVPTRRELAENLGVTEDKVRVWFKNKRARCRRHQR 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LPEHGCKGQEHSD-----SEKASASLPGGSPEDGSLKKKQRRQRTHFTSQQLQELEATF 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPEGGGGNQEPRQQPQPPPEEPAQAAMEGPQPEN----MQPRTRRTKFTLLQVEELESVF 122
                                                          an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                TO 66; 108; 122 AND 132-135
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            1FJL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                     license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19.1%;
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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Pred. No. 5.3e-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; E
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                         dopaminergic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cox J.J.,
                                                                                                                                    a collaboration
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RESULT 9
CRX_BOVIN
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                                                                                                                                                                                                                                 PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
PROSITE; PS50803; OAR; 1.
HOMEOBOX; DNA-binding; Developmental DNA_BIND 62 121 HOMEOBOX
                                                                                      or send an email to license@isb-sib.ch)
                                                                                                 modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                   the
                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                   TISSUE-Retina;
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
                                                                                                                                                                                                                                                                                                                                                                                Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                       Cone-rod homeobox
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00389; HOX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00024; HOMEOBOX. ProDom; PD000010; Homeobox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00046; homeobox;
                                                                                                                                                                                                                                                                                           Zhu X., Craft C.M.;
                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                 Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel.
15-JUN-2002 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003654; Homeo_OAR.
InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 RHTQYPDVPTRRELAENLGVTEDKVRVWFKNKRARCRRHQR
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                                                                                                                                                                             SUBCELLULAR LOCATION: Nuclear (By similarity).
TISSUE SPECIFICITY: RETINA.
SIMILARITY: BELONGS TO THE PAIRED HOMEOBOX FAMILY.
                                                                                                                                ween the Swiss Institute of Bioinfi
European Bioinformatics Institute
                                                                                                                                                                                                              INCLUDING THE OPSIN GENES. ESSENTIAL MAMMALIAN PHOTORECEPTORS.
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                                                                                                                       non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                               Bovinae;
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240
268
302
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41,
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250
272
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40.6%;
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Pred. No. 5.
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                                                                                                 http://www.isb-sib.ch/announce/
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                                                                                                            Usage
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                                                                                                                                                                                                                                                                                                                                                                      Euteleostomi;
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MBL outstation -
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Pfam; PF00046; homeobox; ProDom; PD000010; Homeobo TRANSFAC; T03489;
InterPro; IPR001356; Homeobox.

Homeobox;

SM00389; HOX;

EMBL; AF154123; HSSP; P06601; 1E

IFJL.

AAD34645.1;

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RESULT 10
GSC_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "BICOID" SUBFAMILY.
HSSP; P06601; 1FJL.
TRANSFAC; T04037; -
Genew; HGMC:4612; GSC.
MIM; 138890; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSC_HUMAN
P56915;
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                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
Developmental protein; Nuclear protein; DNA-binding; Homeobox.
DNA_BIND 155 214 HOMEOBOX.
SEQUENCE 252 AA; 27853 MW; 6C0EEC48C084D323 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00046; homeobox; 1.
ProDom; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Molecular cloning of the human homeobox gene goosecoid (GSC) mapping of the gene to human chromosome 14q32.1."; Genomics 21:388-393(194).

-I- FUNCTION: REGULATES CHORDIN (CHRD). MAY PLAY A ROLE IN SPACE OF THE PROPERTY O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Geissert D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Leukocyte;
MEDLINE=94375063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2000 (Rel. 39,
30-MAY-2000 (Rel. 39,
15-JUN-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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DNA_BIND 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transcription regulation; Activator; Homeobox; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homeobox
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      154
                                                                   104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 YAREEVALKINLPESRVQVWFKNRRAKCRQQRQQ 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROGRAMING WITHIN DISCRETE EMBRYONI COMPARTEMENTS DURING ORGANOGENESIS. SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS
RKRRHRTIFTDEQLEALENLFQETKYPDVGTREQLARKVHLREEKVEVWFKNRRAKWRRQ
                                                            --RTRRTKFTLLQVEELESVFRHTQYPDVPTRRELAENLGVTEDKVRVWFKNKRARCRRH 161
                                                                                                                                                                                            GMIPEGGGGNQEPRQQPQPPEEPAQAAMEGPQPENMQP------
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                                                                                                                            GAVPPLGA--QQCSCVPTPPGYEGPGSVLVSPVPHQMLPYMNVGTLSRTELQLLNQLHCR 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPPEEPAQA-AMEGPOPENMOP------RTRRTKFTLLQVEELESVFRHTQYPDV 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGPHYSVNALALSGPSVDLMHPAVSYPSAPRKQRRERTTFTRSQLEELEALFAKTQYPDV 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39,
                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94375063; PubMed=7916327;
De Robertis E.M., Kojis T.,
D., Sparkes R.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR001356; Homeobox.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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HOMEOBOX_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98 F
32253 MW;
                                                                                                                                                                                                                                                                                             18.8%;
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41.5%;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                 Pred.
                                                                                                                                                                                                                                                                                                                        Score 185.5;
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Pred. No. 6.
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512ED6A6DAFBAC19
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                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                 No.
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.2e-07
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                                                                                                                                                                                                                                                                                                                           DB 1;
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                                                                                                                                                                                                                                                                                                                               252;
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RESULT 11
GSC_MOUSE
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                        Query Match
 Matches
            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSC_MOUSE
Q02591;
                                                                                                         Prodom; PD000010; numeous SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=92315328; PubMed=1352187; Blum M., Gaunt S.J., Cho K.W.Y., Bittner D.A., de Robertis E.M.; "Gastrulation in the mouse: the r Cell 69:1097-1106(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSC.
                                                                                                                           Pfam; PF00046; homeobox; 1. ProDom; PD000010; Homeobox; 1.
                                                                                                                                                                                                                   EMBL; M85271; AAA37826.1; -. EMBL; Y13149; CAA73611.1; -. EMBL; Y13150; CAA73612.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98079105; PubMed=9417125;
Danilov V., Blum M., Schweickert A., Campione M., S "Negative autoregulation of the organizer-specific goosecoid";
                                                                                     PROSITE; PS00027; HOMEOBOX_1; 1. PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                           PIR; A42768; A42768.
HSSP; P06601; 1FJL.
                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. The use by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1994 (Rel.
01-FEB-1994 (Rel.
15-JUN-2002 (Rel.
                                                  SEQUENCE
                                                              Developmental protein; Nuclear protein; DNA-binding; Homeobox DNA_BIND 160 219 HOMEOBOX.
                                                                                                                                                                  TRANSFAC; T02047; -. MGD; MGI:95841; Gsc.
                                                                                                                                                                                                                                                                                               modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homeobox
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                                                                                                                                                        nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162
                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Nuclear.
TISSUE SPECIFICITY: IN EARLY G
                                                                                                                                                                                                                                                                                                                                                                                        INDUCTION: BY ACTIVIN. SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biol. Chem. 273:627-635(1998). FUNCTION: GOOSECOID-EXPRESSING REGIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: GOOSECOID-EXPRESSING REGIONS OF THE GASTRULATING MOUSE EGG CYLINDER HAVE ORGANIZER-LIKE ACTIVITY WHEN TRANSPLANTED
                                                                                                                                                                                                                                                                                                                                                                                                                    AND BODY WALL.
                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE SPECIFICITY: IN EARLY GARDORSAL LIP. IN LATER STAGES OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTO XENOPUS EMBRYOS
                                                                                                                                                                                                                                                                                                                                                                            "BICOID" SUBFAMILY.
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 44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein
                                                                                                                                                       IPR001356; Homeobox.
                                                  256 AA;
 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . 28, Created)
. 28, Last sequence update)
. 41, Last annotation update)
goosecoid.
                                                  27979 MW;
             18.8%;
36.1%;
                                                                                                                                                                                                                                                                                                                                                                                         TO THE PAIRED HOMEOBOX FAMILY
16;
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             Pred. No.
                         Score 185.5;
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                                                  3639FB059AC3DB9E CRC64;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                             GASTRULATION, DEVELOPMENT
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             6.8e-07;
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                         DB 1;
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37;
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 Indels
                         Length
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                   PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
PROSITE; PS50803; OAR; 1.
                                                                                                              SMART; SM00389; HOX; 1
                                                                                                                                       Pfam; PF00046; homeobox; 1.
ProDom; PD000010; Homeobox;
                                                                                                                                                                                          InterPro; IPR003654; Homeo_OAR
InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                               Genew;
                                                                                                                                                                                                                                                                                                         EMBL; 297200; CAB10073.1; -. EMBL; 297200; CAB10074.1; -. EMBL; 895929; AAA60085.1; -. HSSP; P06601; 1FJL.
                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    binding activity of serum r
Science 257:1089-1095(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Grueneberg D.A., Natesan S., Alexandre C., Gilman M.Z., "Human and Drosophila homeodomain proteins that enhance binding activity of serum response factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92376525; PubMed=1509260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 19-197 FROM N.A. (ISOFORM PMX1-A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: ACTS AS A TRÂNSCRIPTIONAL REGULATOR OF MUSCLE CREATINE KINASE (MCK) AND SO HAS A ROLE IN THE ESTABLISHMENT OF DIVERSE MESODERMAL MUSCLE TYPES. THE PROTEIN BINDS TO AN A/T-RICH ELEMENT IN THE MUSCLE CREATINE ENHANCER (BY SIMILARITY).

SUBCELLULAR LOCATION: Nuclear.
SUBCELLULAR PRODUCTS: 2 ISOFORMS; PMX1-A AND PMX1-B (SHOWN ALTERNATIVE PRODUCTS: 2 ISOFORMS; PMX1-A AND PMX1-B (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
SIMILARITY: BELONGS TO THE PAIRED HOMEOBOX FAMILY.
SIMILARITY: CONTAINS 1 HOMEOBOX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                             HGNC: 9142; PMX1.
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     DNA-binding; Developmental
                                                                                                                                       Homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  license agreement (See http://www.isb-sib.ch/announce/
  protein;
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  Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          enhance the
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protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a collaboration
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   "rHox: a
J. Cell.
                                                                                                                                                                                                                                                                         "MHOX: a mesodermally restricted homeodomain protein that binds an essential site in the muscle creatine kinase enhancer.";
Development 115:1087-1101(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                PMX1_MOUSE STANDARD; PRT; 245 AA.
P43271; Q02810;
01-FEB-1995 (Rel. 31, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Paired mesoderm homeobox protein 1 (PRX-1) (Paired related homeobox protein 1) (Homeobox protein MhoX) (Homeobox protein K-2) (Rhox).
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VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; NCBI_TaxID=10090, 10116;
                           Morrison N.A.;
                                     Hu Y., Flanagan J.,
                                                  MEDLINE=96340959;
                                                             SPECIES=Rat;
                                                                                                           cloning
                                                                                                                                                                    SEQUENCE FROM N.A. (PMX1-A ISOFORM)
                                                                                                                                                                                          "Genomic organization and chromosome homeobox gene Pmx.";
Genomics 19:334-340(1994).
                                                                                                                                                                                                                              Kern M.J.,
                                                                                                                                                                                                                                                                                                                                                  SPECIES-Mouse;
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (PMX1-A ISOFORM).
                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse), and Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                              PRRX1 OR PMX1 OR PMX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                        SEQUENCE FROM N.A.
                                                                                                 Nucleic
                                                                                                                     "A novel murine homeobox gene isolated
                                                                                                                                    Kern
                                                                                                                                              MEDLINE=93027261;
                                                                                                                                                                                                                                         MEDLINE=94245205; PubMed=7910581;
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (PMX1-A ISOFORM).
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                                                                                                                                M.J., Witte D.P., Valerius M.T.,
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49; Conser
                                                                                     strategy.";
anids Res. 20:5189-5195(1992).
  Biochem.
                                                                                                                                                                                                                              Argao E.A., Birkenmeier E.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  245
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94 15:
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                                                                                                                                                          STRAIN=CD-1
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gene expressed in osteoblastic cells."; 59:486-497(1995).
                                                                                                                                            PubMed=1383943;
                                                 PubMed=8749718;
                                                                       (PMX1-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      153
235
197
245
                                      Brennan D.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27296 MW;
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3 HOMEOBOX.
                                                                          ISOFORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27;
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Pred. No. 7.7e-07;
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SAMATYSATCANNSPAQGINMANSIANLRLKAKEYSLQRNQ
VPTVN -> RSSSLPRCCLHEGLHNGF (IN ISOFORM
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                                      Zhou
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                                      K.W.,
                                                                                                                     Potter S.S., specific PCI
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                                                                                                                                                                                                                   murine
                                      J.A.,
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Best Local Similarity
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EMBL; U03873; L
EMBL; X59725; C
EMBL; S82911; L
HSSP; P06601;
     AL_DROME Q06453;
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00389; HOX;
PROSITE; PS00027; HON
PROSITE; PS50071; HON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSFAC; T02060; -. TRANSFAC; T02061; -. TRANSFAC; T02966; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProDom; PD000010; Homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003654; Homeo_OAR.
InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:97712;
                                                                                                           113
                                                                                                                                           122
                                                                                                                                                                             62
                                                                                                                                                                                                               72
                                                                                                                                                                                                                                                                          31 SSAEGHVGQGAPGLMGNMNPEG------GVNHENGMNRDGGMIP-----EGG
                                                                                                                                                                                                                                               N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MUSCLE, HEART AND UTERUS.
DEVELOPMENTAL STAGE: EXPRESSED DURING CARDIOGENESIS.
SIMILARITY: BELONGS TO THE PAIRED HOMEOBOX FAMILY.
SIMILARITY: CONTAINS 1 HOMEOBOX DOMAIN.
SIMILARITY: CONTAINS 1 OAR DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MESODERMAL MUSCLE TYPES: THE PROTEIN BINDS TO AN A/T-RICH ELEMENT IN THE MUSCLE CREATINE ENHANCER.

SUBCELLULAR LOCATION: NUCLEAR:
ALTERNATIVE PRODUCTS: 2 ISOFORMS; PMX1-A AND PMX1-B (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN MESODERMALLY DERIVED CELL TYPES. DURING EMBRYOGENESIS, HIGHEST LEVELS OF EXPRESSION ARE FOUND IN THE MESENCHYME AND PRECARTILAGE ELEMENTS OF THE FACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: ACTS AS A TRANSCRIPTIONAL REGULATOR OF MUSCLE CREATINE KINASE (MCK) AND SO HAS A ROLE IN THE ESTABLISHMENT OF DIVERSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AND HIND LIMBS.
                                                                                                     FERTHYPDAFVREDLARRVNLTEARVQVWFQNRRAKFRRNER-AMLANK 160
                                                                                                                                         FRHTQYPDVPTRRELAENLGVTEDKVRVWFKNKRARCRRHQRELMLANE 170
                                                                                                                                                                                                                                           TSSYGHVLERQPALGGRLDSPGNLDTLQAKKNFSVSHLLDLEEAGDMVAAQADESVGEAG
                                                                                                                                                                           RSLLESPGLTSGSDTPQQD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS00027; HOMEOBOX_1; 1.
PS500071; HOMEOBOX_2; 1.
PS50803; OAR; 1.
: DNA-binding; Developmental protein; Nuclear protein; ive splicing; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                   245
                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAA39672.1; -.; AAC52139.1; -.; CAA42410.1; -.; AAB46839.1; -.
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                                                                                                                                                                                                         -GGNQEPRQQPQPPPEEPAQAAMEGPQPENMQPRTRRTKFTLLQVEELESV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             homeobox;
                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prrx1.
                                                                                                                                                                                                                                                                                                                                                                                                                                   153
235
197
245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IN THE ADULT, EXPRESSION IS RESTRICTED TO SKELETAL
                                                                                                                                                                                                                                                                                                                                                                                   27269 MW;
                                                                                                                                                                                                                                                                                                                               18.7%;
                                                                                                                                                                                                                                                                                                               27;
                                                                                                                                                                         -----NDQLNSEEKKKRKQRRNRTTFNSSQLQALERV 112
                                                                                                                                                                                                                                                                                                                               Score 184.5; DB 1
Pred. No. 7.7e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OAR.
                                                                                                                                                                                                                                                                                                                                                                                                                VPTVN -> RSSSLPRCCLHEGLHNGF (IN ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                 PHOSPHORYLATION (POTENTIAL).
SAMATYSATCANNSPAQGINMANSIANLRLKAKEYSLQRNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HOMEOBOX.
                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                   FF867F0D856E1115 CRC64;
                                                                                                                                                                                                                                                                                                               Mismatches
                       408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            There are no rest
                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                               54;
                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                 245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a collaboration
                                                                                                                                                                                                                                                                                                               39;
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                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                           61
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                                                                                                                                                                                                                                                                                                               5
     CC. IN THE MAGINAL AND DISTAL
CC. PATTERN ELEMENTS IN A SUBSET OF APPENDAGES. APPEARS ALSO TO HAVE A
CC. PATTERN ELEMENTS IN A SUBSET OF APPENDAGES. APPEARS ALSO TO HAVE A
CC. PATTERN ELEMENTS IN A SUBSET OF APPENDAGES. APPEARS ALSO TO HAVE A
CC. PATTERN ELEMENTS IN A SUBSET OF APPENDAGES. APPEARS ALSO TO HAVE A
CC. PATTERN IN SIZE OF THE ARISTALESS MUTANTS
CC. PATTERN IN SIZE OF THE ARISTAL CLAWS, IRREGULARITIES
CC. OF THE WING BLADE.
CC. IN GENEROLEURAL BRISTLES AND OF THE WING VEIN, AND A BENDING
CC. IN GENEROLEURAL PATTERNS IN HEAD, THORAX AND BADOMEN AND IN AN
CC. IN GENEROLEURAL PATTERNS IN HEAD, THORAX AND ABDOMEN AND IN AN
CC. IN GENEROLEURAL PATTERN IN THE ANTENIOR INTESTINAL TRACT.
CC. IN GENEROLEURAL STAGE: FIRST EXPRESSED IN 4-8 HR-OLD EMBRYOS, PEAKS
CC. IN GENEROLEURAL STAGE: IN THE HEAD REGION, DETECTED AT STAGE 10 IN THE
CC. LARVAL STAGE. IN THE HEAD REGION, DETECTED AT STAGE 10 IN THE
CLARVAL STAGE. IN THE HEAD REGION, DETECTED AT STAGE 10 IN THE
CLARVAL STAGE: IN THE HEAD REGION, DETECTED AT STAGE 11 IN THE
CLARVAL STAGE: IN THE INTESTINAL TRACT BEGINS AT STAGE 13,
CC. THE PROSPECTIVE ANTENNAL AND MANDIBULAR SEGMENT. IN THE ENDIDERMIS,
CC. PATCHES. EXPRESSION IN THE INTESTINAL TRACT BEGINS AT STAGE 13,
CC. CONTINUES THROUGH STAGES 14 AND 15 IN THE ENDODERM OF THE ANTERIOR
CC. MIDGUT AND AT STAGE 15, SEGUN THE PROSPERIOR END. EXPRESSION
CC. HIADDE THORAX, CLAW ORGAN, ANTENNA, SCUTELLUM AND WING
CC. HIADDE
DOMAIN
DOMAIN
DOMAIN
                                                                                PROSITE; PS00027; HOMEOBOX_1; PROSITE; PS50071; HOMEOBOX_2; PROSITE; PS50803; OAR; 1
                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schneitz K., Spielmann P., Noll M.; "Molecular genetics of aristaless, a in the morphogenesis of proximal and subset of appendages in Drosophila."; Genes Dev. 7:114-129(1993)
                                                                                                                                                      PRINTS; PR00031; HTHREPRESSR. ProDom; PD000010; Homeobox; 1.
                                                                                                                                                                                    Pfam; PF00046; homeobox; 1. PRINTS; PR00024; HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BLADE.

-i- SIMILARITY: BELONGS TO THE PAIRED HOMEOBOX FAMILY.

-i- SIMILARITY: CONTAINS 1 HOMEOBOX DOMAIN.

-i- SIMILARITY: CONTAINS 1 OAR DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
                                                                                                                                         SMART; SM00389; HOX;
                                                                                                                                                                                                                                                                           FlyBase; FBgn0000061; al.
                                                                                                                                                                                                                                                                                                             EMBL; L08401; AAA28840.1;
                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                 entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Muscomorpha; Eph
NCBI_TaxID=7227;
                                                     DNA_BIND
                                                                   Homeobox;
                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                             HSSP; P06601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93138380; PubMed=8093690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homeobox protein
                                                                                                                                                                                                                        IPR000047; HTH_repressr.
IPR003654; Homeo_OAR.
IPR001356; Homeobox.
                                                                     DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aristaless.
 144
391
283
360
                                                                                                                                                                                                                                                                                                                                                            license agreement
                                                                   Developmental protein;
                                   OAR.
   GLN/PRO-RICH
                                                     HOMEOBOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   update)
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(See http://www.isb-sib.ch/announce/

and

restrictions on

no way EMBL

a collaboration

outstation

Nuclear

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RESULT 15
ALX4_HUMAN
ALD DATE OF THE PROPERTY OF TH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALX4_HUMAN
Q9H161; Q9H1
16-OCT-2001
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                               "Haploinsufficiency of the human homeobox gene ALX4 causes skull ossification defects.";
Nat. Genet. 27:17-18(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20578741; PubMed=11137991; Mavrogiannis L.A., Antonopoulou I., Bax
Sugayama S.M., Salamanca A., Wall S.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                         Nagase T., Nakayama M., Nakajima D., Kikuno R., Ohara O.; "Prediction of the coding sequences of unidentified human The complete sequences of 100 new cDNA clones from brain v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The ALX4 homeobox gene is mutated in patients with defects of the skull (foramina parietalia permagna, J. Med. Genet. 37:916-920(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ĕ
                                                                                                                                                                                                                                                                MEDLINE=21245130; PubMed=11347906;
                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sugayama S.M.,
Wilkie A.O.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wuyts W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., VARIANT PFM2 P
MEDLINE=20558895; PubMed=11106354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Haploinsufficiency of ALX4 as a potential cause of parietal foramina in the 11pl1.2 contiguous gene-deletion syndrome."; Am. J. Hum. Genet. 67:1327-1332(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shaffer L.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WEDLINE-20489877; PubMed-11017806; Wu Y.-Q., Badano J.L., McCaskill C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homeobox protein
ALX4 OR KIAA1788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Homeobox protein aristaless-like 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-0CT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62
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                                                                                                                  large Proteins in vitro.";
Res. 8:85-95(2001).
FUNCTION: TRANSCRIPTION FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hul
                    SUBCELLULAR LOCATION: Nuclear (By similarity). TISSUE SPECIFICITY: EXPRESSION IS LIKELY TO BE
                                                                    DEVELOPMENT.
SUBUNIT: BINDS DNA (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTNSPVSDGNSDCEADEYAPK----RKQRRYRTTFTSFQLEELEKAFSRTHYPDVFTREEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROOPOPPEEPAQAAMEGPOPENMOPRTRRTKFTLLQVEELESVFRHTQYPDVPTRREL
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408 AA;
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  PARIETAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD; P
Q9HAY9; Q96JN7;
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43644 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANTS R-35 AND P-102,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18.6%;
  BONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homfray T., Rasore-Quartino A., Vanhoenacker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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Pred. No. 1.6e-06;
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; 99F5C8CF787EF99F CRC64;
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permagna, OMIM 168500).";
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                                                                                                                                                                                         which code
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EMBL; AF308822; AAK38835.1;
EMBL; AF308823; AAK38835.1;
EMBL; AF308824; AAK38835.1;
EMBL; AF308825; AAK38835.1;
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PROSITE; PS00027; HOME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SIMILARITY: BELONGS TO THE PAIRED HOMEO
-1- SIMILARITY: CONTAINS 1 HOMEOBOX DOMAIN.
-1- SIMILARITY: CONTAINS 1 OAR DOMAIN.
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PROSITE; PS50803; OAR; 1.
HOmeobox; DNA-binding; Developmental
Transcription regulation; Activator;
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                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00046;
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InterPro; IPR001356;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ERRONEOUS SINGLE-NUCLEOTIDE DELETIONS
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                                             DGSLKLQEGSSGHSAALQVPCYAKESSLGEPELPPDSDTVGMDSSYLSVKEAGVKGPQDR
                                                                     DGGM-IPEGGGGNQEPRQ---
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                       ----PENMQ-----PRTRRTKFTLLQVEELESVFRHTQYPDVPTRRELAENLGV
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AJ279075;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pean Bioinformatics Institute. The
non-profit institutions as long
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/FTId=VAR_010785.
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) -> N (IN REF. 1)
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Polymorphism; Dis
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Search completed: April 28, 2003, 21:14:05
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             No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.
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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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US-08-232-463-1
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                                                                                                                                                                                                                                                                        RESULT 2
US-08-710-249-3
                                                                                                                                                                       Sequence 3, Application US/08710249 Patent No. 5858777 GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junii
APPLICANT: Andrews, William H.
APPLICANT: Adams, Robert R.
APPLICANT: Adams, Robert R.
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326 488 548 446 608 506 668		
	SULT 1 -09-129-888-1 -09-129-888-1 Sequence 1, Applicati Patent No. 6063912 GENERAL INFORMATION: APPLICANT: CHUN, JON APPLICANT: HAN, YUN TITLE OF INVENTION: FILE REFERENCE: 1942 CURRENT APPLICATION CURRENT FILING DATE: NUMBER OF SEQ ID NOS SOCTWARE: WordPerfec ILNGTH: 87 TYPE: DNA ORGANISM: mouse -09-129-888-1 Query Match Best Local Similarity Matches 131; Conser	399.22444.88827772
ACGAACTO COMMENT COMME	8-1 Application 6063912 FORMATION: CHUN, YUN JOOG Y HAN, YUN JOOG INVENTION: Pla RENCE: 1942/29 PPLICATION NUM ILING DATE: 19 SEQ ID NOS: 6 WordPerfect 6 1 B77 B77 B877 B877 B877 B877 A : mouse B-1 B-1 B-1 A Similarity Similarity 31; Conservat	6.888666666666666666666666666666666666
CGGCGCAC AGACGCAC CAATACCAC CGCTACCC AAAGTGCG AAAGTGCG ATGCTCCGC ATGCTCCGC	on US/ g Yoon Jeong Placen NUMBER 1998- : 6 t 6.1 t 6.1 t 6.1	467 1030 11935 11995 4403765 4403765 4403765 4403765 4477 4425 4425 292
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CAGCCACGAACTCGGCGCACGAAGTTCACGCTGTTGCAGGTGGAGGAGGACTTGGAAAGTGTT	888B Ophoblast-spec O9/129,888B WS WS WS Score 71; DB Pred. No. 4.6e; Mismatches	US-08-712-948-6 US-09-055-117-7 US-09-055-117-7 US-08-425-069-3 US-08-137-840A-1 5215895-1 US-09-133-840A-1 5215895-1 US-09-397-787-19 US-08-785-420-1 US-09-319-648-22 US-08-642-255-48 US-08-642-255-48 US-08-642-255-48 US-08-642-255-48 US-09-135-994-1 US-09-344-529-8 ALIGNMENTS
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                                                                   Sequence 3, Application US/09220157A Patent No. 6300110
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                                                       GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 4080 base pairs
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/583,808
FILING DATE: 05-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/003,492
FILING DATE: 08-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION: NAME: Storella, John R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
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LOCATION:
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                        TCCGGAAGAAGCAGCG 626
                                                                                                                                                                                                      GTAGGCGACATCAGAG 510
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                                                                                                                                                                                                                                                                                                        TGGAAAAGACCTTCCAGAAGACTCACTACCCAGATGTGGTGATGCGTGAGAGGCTGGCCA 550
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                                                   INFORMATION:
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Storella, John R.
Storella, 32,944
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Andrews, William H
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                               Villeponteau, Bryant
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Pred. No. 2.3e-05;
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Best Local Similarity
Matches 109; Conserv
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INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER: US 60/003,492
FILING DATE: 08-SEP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
 611
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PRIOR APPLICATION DATA:
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                                                                                                                                                                     375 TGGAAAGTGTTTTCCGACACACTCAATACCCTGATGTGCCCACAAGAAGGGAACTTGCCG 434
                                                                                                                                                                                                                         431 CCCAGCACCGCAAACAACGTCGCAGCCGCACAGCGTTCACGGCTCAGCAGCTCGAGGCCC 490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/710,249 FILING DATE: 13-SEP-1996 APPLICATION NUMBER: US 08/583,808 FILING DATE: 05-JAN-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Storella, John R. REGISTRATION NUMBER: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                           AAAACTTAGGTGTGACTGAAGACAAAGTGCGGGTTTGGTTTAAGAATAAAAGGGCCAGAT 494
TCCGGAAGAAGCAGCG
                                  GTAGGCGACATCAGAG 510
                                                                       TGTGCACCAACCTGCCTGAGGCCCGGGTGCAGGTGTGGTTCAAGAACCGCCGGGCCAAGT 610
                                                                                                                                               TGGAAAAGACCTTCCAGAAGACTCACTACCCAGATGTGGTGATGCGTGAGAGGCTGGCCA 550
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Methods and Reagents for Regulating: Telomere Length and Telomerase Actiss: 26
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55.6%;
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RESULT 4 US-08-957-351-6

Sequence 6, Application US/08957351 Patent No. 6306586

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                                                                                   RESULT 5
US-08-957-351-5
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                 Sequence 5, Application US/08957351
Patent No. 6306586
GENERAL INFORMATION:
APPLICANT: Semina, Elena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 9.8%;
Best Local Similarity 52.9%;
Matches 148; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 6:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: UII
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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APPLICANT: Murray, Jeffrey C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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ADDRESSEE: FOLEY, HC
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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NAME: Arnold, Beth E.
     APPLICANT:
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                                                                                                                                                                                                                                                                                                             280
                                                                                                                                                                                                                                                        400 ATACCCTGATGTGCCCACAAGAAGGGAACTTGCCGAAAACTTAGGTGTGACTGAAGACAA 459
                                                                                                                                                                                                                                                                                                                                                           141 GCTGCCCGGCGCTCCCCAGAGGACGGTTCGC----TGAAAAAAAAGAAGCAGCGGCGGCA
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STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                       CGTGCGGGTGTGGTTCAAGAACCGGCGCGCCCAAATGGCGG
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                                                                                                                                                                                                                       CTACCCCGACATGAGCACGCGCGAGGAGATCGCCGTGTGGACAAACCTCACCGAGGCCCG 314
                                                                                                                                                                                                                                                                                         GCGCACGCACTTCACCAGCCAGCAGCTACAGGAGCTAGAGGCGACCTTCCAGAGGAACCG
                                                                                                                                                                                                                                                                                                                                                                                            GGAGCCGGCCCAGGCGGCCATGGAGGGTCCGCAGCCCGAGAACATGCAGCCACGAACTCG 339
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                Elena
Jeffrey C
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Pred. No. 2.1e-05;
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                                                                                                                                                                                                                  RESULT 6
US-08-958-642-3
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US-08-957-351-5
                                                                                                                                                                            Sequence 3, Application Patent No. 5948623
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Best Local Similarity
Matches 148; Conserv
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TELEFAX: 61/-02
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
SEQUENCE 1017 base pairs
TITLE OF INVENTION: NOVEL METHO)
TITLE OF INVENTION: DIFFERENTIAN
NUMBER OF SEQUENCES: 16
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                          GENERAL INFORMATION:
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FILING DATE: 24-OCT 1997
CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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CITY: Boston
STATE: MA
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ZIP: 02109-2170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCGCACGAAGTTCACGCTGTTGCAGGTGGAGGGGAGCTGGAAAGTGTTTTCCGACACACTCA 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATACCCTGATGTGCCCACAAGAAGGGAACTTGCCGAAAACTTAGGTGTGACTGAAGACAA 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                GCGCACGCACTTCACCAGCCAGCAGCTACAGGAGCTAGAGGCGACCTTCCAGAGGAACCG 257
                                                                                                                                                                                                                                                                                           CGTGCGGGTGTGGTTCAAGAACCGGCGCGCCCAAATGGCGG
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                                                                             NOVEL METHOD FOR TESTING THE DIFFERENTIATION STATUS IN PANCREATIC CELLS OF A MAMMAL
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Pred. No. 2.1e-05;
0; Mismatches 126;
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US-08-778-394-1
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US-08-778-394-1
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Patent No. 6028184
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
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Best Local Similarity
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                                                                                                                                                                     CLASSIFICATION: 514
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
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SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                 FEATURE
                                                                MOLECULE TYPE:
DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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DESCRIPTION: /desc = "oligonucleotide"
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           NAME/KEY:
LOCATION:
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TOPOLOGY: li
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LOCATION:
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                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STRANDEDNESS: sing
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                                                                                                                                                                                                                                            APPLICATION NUMBER:
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                                                                                                                                                    LENGTH:
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                                                                                                               nucleic acid
EDNESS: single
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163..1470
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                                                              other nucleic acid
/desc = "oligonucleotide"
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55.4%;
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Pred. No. 4.7e-05;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: December 31, INFORMATION FOR SEQ ID NO: 3:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE
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LENGTH: 2481 base pair
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1002 AAGAGAAGAAA 1014
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                                 499 GCGACATCAGAGA 511
                                                                      942 AATAGATCTACCTGAAGCAAGAATACAGGTATGGTTTTCTAATCGAAGGGCCAAATGGAG
                                                                                                                                                                             379
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TOPOLOGY: lir
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                                                                                                                                                                                                                                                                                                                                                                             LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                     CTTAGGTGTGACTGAAGACAAAGTGCGGGTTTGGTTTAAGAATAAAAGGGCCCAGATGTAG 498
                                                                                                                                          GAAAGAGTTTGAGAGGACCCATTATCCAGATGTGTTTGCCCGGGAAAGACTAGCAGCCAA
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IBM PC compatible
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/desc = "oligonucleotide"
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55.4%;
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Pred. No. 4.7e-05;
0; Mismatches 86;
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US-08-957-351-2
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US-08-957-351-2
            Sequence 1, Application US/08957351 Patent No. 6306586 GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT: Semina,
APPLICANT: Murray,
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TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
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FILING DATE: 24-0CT-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ATOOLd, Beth E.
PROTETTATION NUMBER: 25 420
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MEDIUM TYPE: Floppy disk
APPLICANT:
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                                                                                                                                                                                                294 GACCAACCTCACTGAGGCCCGCGTGCGGGTGTGGTTCAAGAACCGGCGCGCCAAGTGGCG 353
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REFERENCE/DOCKET NUMBER: UIA-024.01
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One Post Office Square
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METHODS AND COMPOSITIONS FOR THE
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                                                                                                                                                                                                                                                                                                                                                                                            Score 54.6; DB 4;
Pred. No. 5.8e-05;
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RESULT 11
US-09-636-735A-1
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Best Local Similarity 56.4
                  CURRENT APPLICATION NUMBER: US/09/636,735A
CURRENT FILING DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 1251
TYPE: DNA
                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                 Sequence 1, Applic Patent No. 6416956
                                                                                                                                         APPLICANT: Berg, Patricia TITLE OF INVENTION: No. 64169 FILE REFERENCE: 179.37405X00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 617-832-7000 INFORMATION FOR SEQ ID NO:
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/OFFILING DATE: 24-OCT-1997 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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ZIP: 02109-2170
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Arnold, Beth E.

NITMBER: 35,430
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56.4%;
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METHODS AND COMPOSITIONS FOR THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1392;
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US-08-958-642-1
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                                                                                                                                                                                                                                                     Query Match
Best Local
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Best Local Similarity 51.3
Matches 121; Conservative
                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: December INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: 1i
MOLECULE TYPE:
DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: (285)..(1004)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
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                               401
                                                                                            583
                                                                                                                                                     341 CGCACGAAGTTCACGCTGTTGCAGGTGGAGGAGCTGGAAAGTGTTTTCCGACACACTCAA 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     758
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         274 GCCGGAGGAGCCGGCCCAGGCGGCCATGGAGGGTCCGCAGCCCGAGAACATGCAGCCACG 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08 FILING DATE: December
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
TACCCTGATGTGCCCACAAGAAGGGAACTTGCCCGAAAACTTAGGTGTGGATGAAGACAAA 460
                                                                                            CGGGCTATCTTCTCCCCGGGACAAGCCGAGGCACTGGAGAAAGAGTTTCAGCGTGGGCAG 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCCGCGGCTGTCCCCGGAACCCTCCGAGCGGCGCCCTCAGGCCCCCGCCAAAAAGCTCCG 637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CACTCAATACCCTGATGTGCCCACAAGAAGGGAACTTGCCGAAAACTTAGGTGTGACTGA 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAAGCCGAGGACCATCTACTCCAGCCTGCAGCTGCAGCACCTAAAACCAGCGTTTCCAGCA 697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1275 base pairs
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/desc = "oligonucleotide"
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52.9%;
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51.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08/778,423
er 31, 1996
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Pred. No.
                                                                                                                                                                                                                                                 Score 51.6;
Pred. No. 0.
                                                                                                                                                                                                                  Mismatches
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US-08-778-423A-1
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                                                 Sequence 1, Application Patent No. 6071697 GENERAL INFORMATION: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity Matches 111; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 514
INFORMATION FOR SEQ ID NO:
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APPLICANT:
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TITLE OF INVENTION: DIF
NUMBER OF SEQUENCES: 4
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d
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MOLECULE TYPE: <
DESCRIPTION: ,
APPLICANT:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
.LENGTH: 1275 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/778,394
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                                                                                                                                                                                                                                                                                                                            745
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                                                                                                                                                                                                                                                                                          461
                                                                                                                                                                                                                                                                                                                                                           401 TACCCTGATGTGCCCCACAAGAAGGGAACTTGCCGAAAACTTAGGTGTGACTGAAGACAAA 460
                                                                                                                                                                                                                                                                                                                                                                                             685
                                                                                                                                                                                        865 GAAGCACAGCTGCCAGGTGCTTCCCAGGAC
                                                                                                                                                                                                                         521
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Palanning
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       805 GTGAGGGTTTGGTTTTCTAACAGAAGAGCCAAATGGCGCAAGAGAAAGCTGAAATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      745 TATCCAGATTCAGTGGCCCGTGGGAAGCTGGCTGCCGCCACCTCTCTGCCTGAAGACACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                           CTCGCCAATGAACTACGTGCTGACCCAGAC
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                                                                                                                                                                                                                                                                                                                            TATCCAGATTCAGTGGCCCGTGGGAAGCTGGCTGCTGCCACCTCTCTGCCTGAAGACACG 804
                                                                                                                                                                                                                                                                                                                                                                                             CGGGCTATCTTCTCCCCGGGACAAGCCGAGGCACTGGAGAAAGAGTTTCAGCGTGGGCAG 744
                                                                                                                                                                                                                                                           GTGAGGGTTTGGTTTTCTAACAGAAGAGCCAAATGGCGCAGGCAAGAGAAGCTGAAATGG
                                                                                                                                                                                                                                                                                        GTGCGGGTTTGGTTTAAGAATAAAAGGGCCAGATGTAGGCGACATCAGAGAGAATTAATG
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166..1161
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/desc = "oligonucle"
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 NOVEL METHOD FOR TESTING THE DIFFERENTIATION STATUS IN PA
                                                                                                    US/08778423A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "oligonucleotide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 51.6; DB 3;
Pred. No. 0.00035;
0; Mismatches 99;
                                                                                                                                                                                          894
                                                                                                                                                                                                                       550
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 IN PANCREATIC CELLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: December 31, 11
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1275 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECHLE TUPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/07590894C Patent No. 5342761 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 8.9%;
Best Local Similarity 52.9%;
Matches 111; Conservative
ATTORNEY/AGENT INFORMATION:
NAME: Adder Ph.D., Benjamin A.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5237
                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBEE: US/07/590,894C
FILING DATE: 01-OCT-1990
                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: MacLeod,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          865 GAAGCACAGCTGCCAGGTGCTTCCCAGGAC 894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          521 CTCGCCAATGAACTACGTGCTGACCCAGAC 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             401 TACCCTGATGTGCCCACAAGAAGGGAACTTGCCGAAAACTTAGGTGTGACTGAAGACAAA 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              341 CGCACGAAGTTCACGCTGTTGCAGGTGGAAGGAGCTGGAAAGTGTTTTCCGACACACTCAA 400
                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION:
                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 77010-3095
                                                                                                                                                                                                                                                                                                CITY: Houston
STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/778,423A FILING DATE: December 31, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGGGCTATCTTCTCCCCGGGGACAAGCCGAGGCACTGGAGAAAGAGTTTCAGCGTGGGCAG 744
                                                                                                                                                                                                                                                                                                                                   E: Dr. Benjamin A. Adler
1301 McKinney St. 41st Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PatentIn Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              other nucleic acid
/desc = "oligonucleotide"
                                                                                                                                                                                                                                                                                                                                                                                                                 Carol L A No. 5342761el Onco-Fetal Gene, Gene Product and Uses Therefor % \left( 1\right) =\left\{ 1\right\} =\left\{ 1\right\} 
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Pred. No. 0.00035;
0; Mismatches 99;
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Best Local Similarity 49.8%;
Matches 150; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
ORIGINAL SOURCE:
                                      .556 T 556
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                                                                                                                                                                                                                                                                       376
                                                                                                                                                                                                                                                                                                           426 TGGGGGTAGGCAGATGCCCCTCCAGGGCTCTAGGTTCGCCCCAGCATCGACTGAGGGAACT
663 T 663
                                                                          603 CAGAAGAAACAGGAGGAGGCAACACCAGTCCCTGAACATTTTAGAGGAACATTCGAGTG 662
                                                                                                                                                                                                                                                                                                                                               316 CGAGAACATGCAGCCACGAACTCGGCGCACGAAGTTCACGCTGTTGCAGGTGGAGGAGCT 375
                                                                                                                                                                                                                                                                                                                                                                                     366 GGAGCAGGAACAAAATGAGCCAGTTGCTGAGGGCACTGAGAGCCAGGAGAATGGAAATCC 425
                                                                                                                                                                                                                                                                                                                                                                                                            256 GCAGCAGCCGCAGCCCCCCCCGCAGGAGCCGGCCCAAGGCCCATGGAAGGGTCCGCAGCC 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CELL TYPE: T-cell
CELL LINE: SL12.4 clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INDIVIDUAL ISOLATE: SL12 cell line DEVELOPMENTAL STAGE: Bone marrow-acTISSUE TYPE: Lymphoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: N at nucleotide 838 represents a polyA string
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 713-651-5587
TELEFAX: 713-651-5246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN: AKR1 Jackson
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                                                                                                                                                                                                                                                       GGAAAGTGTTTTCCGACACACTCAATACCCTGATGTGCCCACAAGAAGGGAACTTGCCGA 435
                                                                                                                TAGGCGACATCAGAGAGAATTAATGCTCGCCAATGAACTACGTGCTGACCCAGACGACTG 555
                                                                                                                                                                          AAACTTAGGTGTGACTGAAGACAAAGTGCGGGTTTGGTTTAAGAATAAAAGGGCCAGATG 495
                                                                                                                                                                                                                                 GGAGTCCATTTTGCAGCGCACTAATTCCTTTGATGT---CCCAAGGGAGGATCTTGATAG 542
                                                                                                                                                      ACTGATGGATGCCTGTGTGTCCAGAGTGCAGAATTGGTTTAAGATCAGGAGGGCTGCGGC 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               838 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA to mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 48.2; DB 1; Pred. No. 0.0023;
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Search completed: April 28, 2003, 19:25:28 Job time: 72 secs

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